

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 11, 2000, 06:08:11 ; Search time 15.53 seconds
(without alignments)
1283.098 Million cell updates/sec

Title: US-09-405-940-1
Perfect score: 1664
Sequence: 1 MGTRLLCWAALCLLGADHTG.....AVLVSAVLMMVKKRDSRG 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_65: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1094.5	65.8	307	2 S03716	T-cell receptor be
2	1048.5	63.0	309	2 S18894	T-cell receptor be
3	1036	62.3	306	2 S25118	T-cell receptor be
4	944	56.7	179	2 C25777	T-cell receptor be
5	907	54.5	177	1 RWHUCY	T-cell receptor be
6	856.5	51.5	267	2 P20064	T-cell receptor be
7	772.5	46.4	178	2 PQ0075	T-cell receptor be
8	770	46.3	177	2 B49054	T-cell receptor be
9	763.5	45.9	178	2 PQ0076	T-cell receptor be
10	750	45.1	177	1 RNVVTC	T-cell receptor be
11	741	44.5	173	2 A46547	T-cell receptor be
12	741	44.5	319	1 RWEBB	T-cell receptor be
13	736	44.2	173	1 RWSIC	T-cell receptor be
14	732.5	44.0	174	2 A49828	T-cell receptor be
15	731	43.9	173	1 RWSBC	T-cell receptor be
16	724	43.5	173	2 B46547	T-cell receptor be
17	724	43.5	237	2 A30602	T-cell receptor be
18	710	42.7	173	2 G27579	T-cell receptor be
19	661	39.7	141	2 S03495	T-cell receptor be
20	653	38.2	139	2 S38393	T-cell receptor be
21	632.5	38.0	135	2 S57882	T-cell receptor PS
22	621	37.3	151	2 S24064	T-cell receptor be
23	570	34.3	114	2 PT0733	T-cell receptor be
24	570	34.3	115	2 S22035	T-cell receptor be
25	526.5	31.6	125	2 B45806	T-cell receptor be
26	526	31.6	269	2 I46884	T-cell receptor be
27	510.5	30.7	129	2 S57884	T-cell receptor WI
28	476	28.6	114	2 PT0734	T-cell receptor be
29	476	28.6	115	2 S22038	T-cell receptor be

RESULT 1
S03716
T-cell receptor beta chain precursor (F5) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 05-Nov-1999
C:Accession: S03716
R:Palmer, M.S.; Bentley, A.; Gould, K.; Townsend, A.R.M.
Nucleic Acids Res. 17, 2353, 1989
A:Title: The T cell receptor from an influenza-A specific murine CTL clone.
A:Reference number: S03715; MUID:99202046
A:Accession: S03716
A:Molecule type: mRNA
A:Residues: 1-307 <PAL>
A:Cross-references: EMBL:X14388; NID:g54668; PIDN:CAA32563.1; PID:g54669
C:Keywords: T-cell receptor
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-307/Product: T-cell receptor beta chain #status predicted <MAT>

Query Match 65.8%; Score 1094.5; DB 2; Length 307;
Best Local Similarity 68.6%; Pred. No. 7.6e-78;
Matches 214; Conservative 34; Mismatches 59; Indels 5; Gaps 2;

Qy 1 MGTRLLCWAALCLLGADHTGAGVSQTPSNKYTERGKDVELECDPISGHTALYWRQSLGQ 60
Db 1 MAPRLFLCLVCLFRAEPTNAGVITQPRHKVTGKQEATLWCEPISGHSVFWYRQITVQ 60
Qy 61 GPEFLIYFGGTGAADDGSLPNDREFAVEPEGSVSTLKTORTQGDGAAYLRAGVAGWSS 120
Db 61 GLEFLIYFRNAPIDDSGMPKRFSAQPNOSHSTLKIQTQDQSAVYLCS-SSRTGG 119
Qy 121 YNEQYFGTGLTLEDLKNVFPPEVAFPESEAEISHTQKATLVCLATGFPDPHVELSW 180
Db 121 YNEQYFGTGLTLEDLKNVFPPEVAFPESEAEISHTQKATLVCLATGFPDPHVELSW 179
Qy 181 WYNGKEVHSGVSTDPQPKQEPALNDSRYCLSSRLRSVATFWQNRHFRQCVFGLSE 240
Db 180 WYNGKEVHSGVSTDPQAYKE- - -SNVSYCLSSRLRSVATFWHPRHFRQCVFGLSE 235
Qy 241 NDEWTFQRAKPVQTVSAEAMGRADCGFTSESQOQVLVSATILYELILGKATLVAVLSA 300
Db 236 EDKWPESGPKPVTONISAEAMGRADCGITSASYHQGLVSATILYELILGKATLVAVLSG 295
Qy 301 LVLMAMVKKRDS 312
Db 296 LVLMAMVKKRNS 307

RESULT 2
S18894
T-cell receptor beta chain precursor - human
C:Species: Homo sapiens (man)

Db 295 LVLMAVKKNS 306

RESULTS 4

C25777

T-cell receptor beta-2 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 21-Jan-2000

C:Accession: C25777; B24687

F:Tunnacliffe, A.; Kefford, R.; Millstein, C.; Forster, A.; Rabbitts, T.H.

Proc. Natl. Acad. Sci. U.S.A. 82, 5088-5072, 1985

A:Title: Sequence and evolution of the human T-cell antigen receptor beta-chain genes

A:Reference number: A94053; MUID:85270467

A:Accession: C25777

A:Molecule type: DNA

A:Residues: 1-179 <TUN>

A:Cross-references: GB:M12888

R:Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985

A:Title: Organization and sequences of the diversity, joining, and constant region genes

A:Reference number: A94081; MUID:86094276

A:Accession: B24687

A:Molecule type: DNA

A:Residues: 1-179 <TOY>

C:Genetics:

A:Gene: GDB:TCRB

A:Cross-references: GDB:120405; OMIM:186930

A; introns: 174; 130/11; 136/11; 1/173
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; keywords: T-cell receptor
F; 24-98/Domain: immunoglobulin homology <IMM>

Query Match 56.7%; Score 944; DB 2: Length 179;
Best Local Similarity 100.0%; Pred. No. 1.9e-66;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 EDLKNVPEPPEVAPESEAEIISHTKATLVCLATGTFPDHVELSWWYNGKEVSGVSTDP 195
| | | | | | | | | | | | | | | | | | | | | |
Db 1 EDLKNVPEPPEVAPESEAEIISHTKATLVCLATGTFPDHVELSWWYNGKEVSGVSTDP 60

QY 196 OPLKEOPALNDSRYCLSSRLKVSATFWONPNRHFRCOVFYGLSENDEWTODRAKPVTQI 255
| | | | | | | | | | | | | | | | | | | | | |
Db 61 OPLKEOPALNDSRYCLSSRYEVSATFWONPNRHFRCOVFYGLSENDEWTODRAKPVTQI 120

	QY	VSAEAWGRADCGFTS9SYQQGVLSATILYEILGKATLYAVLSALVLMANVKRDSRG	314
	D6	VSAEAWGRADCGFTS9SYQQGVLSATILYEILGKATLYAVLSALVLMANVKRDSRG	179

RESULT 5
RWHCY
T-cell receptor beta-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 02-Sep-1997
C:Accession: B25777; A02133
R:Tunnacliffe, A.; Kefford, R.; Milstrein, C.; Forster, A.; Rabbitts, T.H.

```

Db      2 LSCKNNHNHWYWRDMGHGLRLIISYDVNSTEKGDVPNG-----YKVS 48

Qy     100 RTEQGD-----SAAYLRAGV--AAGWSSYNEQYFGPGTRLTVLIEDLKNVFPPEVAFFE 150
       |||          |   |   |   |   |   |   |   |   |   |   |   |   |
Db      49 RPSQDFFLTLESASPOTSIVFYFCASSDSNTEVEFFGCKGTRLTVVEDLKTWTPPKVSLFE 108

Qy     151 PSEAEISHTKATILVCLATGFYPDHVELSWWVNGKEYHSGVSTDPQLKPQPALNDSRYC 210
       |||||         |||||         |||||         |||||         |||||         |||
Db      109 PSEAEIAADKOKATILVCARGFFPDHVELSWWVNGKEIRNGVSTDPQAYKES---NNITYC 165
       |||||         |||||         |||||         |||||         |||||         |||

Qy     211 LSSRLRSYATFWQPNRNRHFRCQVGYGLSENDEWTDQRAKPVTOIVSAEAWGRADCGETS 270
       |||||         |||||         |||||         |||||         |||||         |||
Db      166 LSSRLRSYATFWHPNRHRFCQVGYGLTEEDNWSDSPKPTONISAGAWGRADCGITS 225

Qy     271 ESYQGVLSTATILEILLGKATLYAVLSALVLMAMVKRKDS 312
       |||||         |||||         |||||         |||||         |||||         |||
Db      226 ASYQGVLSTATILEILLGKATLYAVLSLVLMVMAMVKRKSS 267
       |||||         |||||         |||||         |||||         |||||         |||

RESULT 7
PQ0075
T-cell receptor beta chain (BTB82 c beta 1) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: PQ0075
R:Tanaka, A.; Ishiguro, N.; Shinagawa, M.
submitted to JIPID, May 1990
A:Description: Sequence analysis of bovine T-cell receptor beta chain genes.
A:Reference number: JQ0472
A:Accession: PQ0075
A:Molecule type: mRNA
A:Residues: 1-178 <TAN>
A:Experimental source: T cell
A:Genetics:
C:Gene: BTB82 c beta 1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: receptor
F:24-98/Domain: immunoglobulin homology <IMX>

Query Match           46.4%: Score 772.5; DB 2; Length 178;
Best Local Similarity 82.0%: Pred. No. 4e-53;
Matches 14%; Conservative 15; Mismatches 16; Indels 1; Gaps

Qy     136 EDLNKVPPEVAVPEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEYHSGVSTDP 195
       |||         |||||         |||||         |||||         |||||         |||
Db      1 DDLGVHPKPVAVPEPSEAEISRQKATLVCLATGFYPDHVELTWVNRKQVTGTVDTP 60

Qy     196 QPLKEQPALNDSRYCLSSLRVSATFWQPNRHHFRCCQVFVGLSENDEW-TQDRAPVQTQ 254
       :|||         |||||         |||||         |||||         |||||         |||
Db      61 EPYKEDPARDDSRVCLSSLRVATFAFWHPNRHHFRCCQVFVGLTQQDWEEQDRAPVQTQ 120

Qy     255 IVSAEAWGRADCGETSSYQGVLSTATILELLGKATLYAVLSALVLMAMVKRKDS 312
       |||||         |||||         |||||         |||||         |||||         |||
Db      121 NISAEAWGRADCGVTSASYQGVLSTATILELLGKATLYAVLSALVLMAMVKRKES 178

RESULT 8
B49054
B49054
T-cell receptor beta chain C region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B49054
R:Thome, A.; Saalmuller, A.; Pfaff, E.
Eur. J. Immunol. 23, 1005-1010, 1993
A:Title: Molecular cloning of porcine T cell receptor alpha, beta, gamma and delta genes.
A:Reference number: A49054; MUID:93238851
A:Accession: B49054
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-177 <THO>
A:Cross-references: GB:L21159; NDB:g309798; PIDN:AAA65021.1; PID:g309799
A>Note: sequence extracted from NCBI backbone (NCBIP:130286)
```


A:Reference number: A94052; MUID:85242712

A:Accession: A94052

A:Molecule type: mRNA

A:Residues: 1-319 <ANG>

R:Wage, R.

Submitted to the Protein Sequence Database, April 1987

A:Reference number: A94616

A:Contents: corrections to residues 79-83 and 104-105

A:Accession: A94616

A:Molecule type: mRNA

A:Residues: 79-83,104-105 <MAC>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: glycoprotein; heterotetramer; T-cell receptor; transmembrane protein

F:166-240/Domain: immunoglobulin homology <IMM>

F:292-313/Domain: transmembrane #status predicted <TM>

F:314-318/Domain: intracellular #status predicted <INT>

F:147,164,254,262/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.5%; Score 741; DB 1; Length 319;

Best Local Similarity 76.5%; Pred. No. 2.3e-50;

Matches 140; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 130 TRUTVLEDKNVPEVAVPEPSEAEISHTQKATLVCLATGYPDHVELSWVNGKEVHS 189

Db 137 TPHFPEDLANVAPQVVPDPSEAEINKTKATLVCLAKDFPDHVELSWVNGKEVHN 196

QY 190 GVSTDPQPLKEQPALNDSRYCLSSRLRVSAFWQNPNNHFRFCQVQYGLSENDEWTFQDRA 249

Db 197 GVSTDPQPYKQPKSDHSKSKYCLSSRLRVSAFAWHNPNHFRFCQVQYGLTDDDEWTYNS 256

QY 250 KPVTQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKATLYAVLSALVLMAMVKR 309

Db 257 KPTQNTSATNTRADCGISASYYQQGVLSATVLYEILLGKATLYAVLSALVLMAMVKR 316

QY 310 KDS 312

Db 317 KDS 319

RESULT 13

RWMS1C

T-cell receptor beta-1 chain C region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 16-Aug-1996

C:Accession: B93336; A93325; A23572; A02135

R:Gascoigne, N.R.J.; Chien, Y.; Becker, D.M.; Kavalier, J.; Davis, M.M.

Nature 310, 387-391, 1984

A:Title: Genomic organization and sequence of T-cell receptor beta-chain constant- and

A:Reference number: A93336; MUID:84270704

A:Accession: B93336

A:Molecule type: DNA

A:Residues: 1-173 <GAS>

A:Cross-references: GB:M26053

A:Experimental source: strain B10.A, cytotoxic T lymphocyte

R:Hedrick, S.M.; Nielsen, E.A.; Kavalier, J.; Cohen, D.I.; Davis, M.M.

Nature 308, 153-158, 1984

A:Title: Sequence relationships between T-cell receptor polypeptides and immunoglobulins

A:Reference number: A93325; MUID:84142271

A:Accession: A93325

A:Molecule type: mRNA

A:Residues: 1-69, 'H', 71-173 <HED>

A:Cross-references: GB:K01080

A:Experimental source: clone 86T1

R:Morinaga, T.; Fotedar, A.; Singh, B.; Wegmann, T.G.; Tamaoki, T.

Proc. Natl. Acad. Sci. U.S.A. 82, 8163-8167, 1985

A:Title: Isolation of cDNA clones encoding a T-cell receptor beta-chain from a beef insu

A:Reference number: A94078; MUID:86068062

A:Accession: A23572

A:Molecule type: mRNA

A:Residues: 1-173 <MOR>

A:Cross-references: GB:M11456

A:Note: the authors translated the codon TAT for residue 134 as Val

C:Genetics:

A:Introns: 1/1; 126/1; 132/1; 163/3

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: glycoprotein; heterotetramer; receptor; T-cell; transmembrane protein

F:24-94/Domain: immunoglobulin homology <IMM>

F:152-168/Domain: transmembrane #status predicted <TM>

F:169-173/Domain: intracellular #status predicted <INT>

F:31-71/Disulfide bonds: #status predicted

F:67,116/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.2%; Score 736; DB 1; Length 173;

Best Local Similarity 79.1%; Pred. No. 2.6e-50;

Matches 140; Conservative 16; Mismatches 17; Indels 4; Gaps 1;

QY 136 EDLKNVFPPEVAVFPPEPSEAEISHTQKATLVCLATGYPDHVELSWVNGKEVHSGVSTDP 195

Db 1 EDLRNVTTPKVSIFPEPSKAEIAKOKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDP 60

QY 196 QPLKEQPALNDSRYCLSSRLRVSAFWQNPNNHFRFCQVQYGLSENDEWTFQRAKPVQTQI 255

Db 61 QAYKE-----SNYSYCLSSRLRVSAFWQNPNNHFRFCQVQYGLSEDKWPEGSPKPVTON 116

QY 256 VSAEAWGRADCGFTSESYQQGVLSATILYEILLGKATLYAVLSALVLMAMVKRSDS 312

Db 117 ISAEAWGRADCGITTSASYQQGVLSATILYEILLGKATLYAVLSALVLMAMVKRSDS 173

RESULT 14

A49828

T-cell receptor beta chain C region (Cbeta1) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C:Accession: A49828

R:Blankenhorn, E.P.; Stranford, S.A.; Smith, P.D.; Hickey, W.F.

Eur. J. Immunol. 21, 2033-2041, 1991

A:Title: Genetic differences in the T cell receptor alleles of LEW rats and their enc

A:Reference number: A49828; MUID:91364772

A:Accession: A49828

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-174 <BLA>

A:Cross-references: GB:S60762; NID:g235079; PIDN:AAB19719.1; PID:g235080

A:Experimental source: Lewis

A:Note: sequence inconsistent with nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:60762, NCBI:60764)

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: T-cell receptor

F:24-95/Domain: immunoglobulin homology <IMM>

Query Match 44.0%; Score 732.5; DB 2; Length 174;

Best Local Similarity 78.0%; Pred. No. 4.9e-50;

Matches 138; Conservative 15; Mismatches 21; Indels 3; Gaps 1;

QY 136 EDLKNVFPPEVAVFPPEPSEAEISHTQKATLVCLATGYPDHVELSWVNGKEVHSGVSTDP 195

Db 1 EDLKTVPKVSIFPEPSEAEIAKOKATLVCLARGFFPDHVELSWVNGKEIRNGVSTDP 60

QY 196 QPLKEQPALNDSRYCLSSRLRVSAFWQNPNNHFRFCQVQYGLSENDEWTFQRAKPVQTQI 255

Db 61 QATKES---NNITYCLSSRLRVSAFWQNPNNHFRFCQVQYGLTEEDNWSDESPKPVTON 117

QY 256 VSAEAWGRADCGFTSESYQQGVLSATILYEILLGKATLYAVLSALVLMAMVKRSDS 312

Db 118 ISAEAWGRADCGITTSASYQQGVLSATILYEILLGKATLYAVLSALVLMAMVKRSDS 174

RESULT 15

RWMSBC

T-cell receptor beta-2 chain C region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Aug-1984 #sequence_revision 28-Feb-1986 #text_change 05-Sep-1997
C:Accession: A93336; B93333; A02134
R:Gascoigne, N.R.J.; Chien, Y.; Becker, D.M.; Kavalier, J.; Davis, M.M.
Nature 310, 387-391, 1984
A:Title: Genomic organization and sequence of T-cell receptor beta-chain constant- and j
A:Reference number: A93336; MUID:84270704
A:Accession: A93336
A:Molecule type: DNA
A:Residues: 1-173 <GAS>
A:Experimental source: strain B10.A, cytotoxic T lymphocyte
R:Saïto, H.; Kranz, D.M.; Takagaki, Y.; Hayday, A.C.; Eisen, H.N.; Tonegawa, S.
Nature 309, 757-762, 1984
A:Title: Complete primary structure of a heterodimeric T-cell receptor deduced from cDNA
A:Reference number: A93333; MUID:84245824
A:Accession: B93333
A:Molecule type: mRNA
A:Residues: 1-49, 'R', 51-69, 'H', 71-173 <SAI>
A:Experimental source: BALB.B, clone 2C, cytotoxic T lymphocyte
C:Genetics:
A:Introns: 1/1; 126/1; 132/1; 163/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; receptor; T-cell; transmembrane protein
F:24-94/Domain: immunoglobulin homology <IMM>
F:147-168/Domain: transmembrane #status predicted <TMM>
F:169-173/Domain: intracellular #status predicted <INT>
F:67,116/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 43.9%; Score 731; DB 1; Length 173;
Best Local Similarity 78.5%; Pred. No. 6.4e-50;
Matches 139; Conservative 16; Mismatches 18; Indels 4; Gaps 1;

QY 136 EDLKNVPEPEVAVPEPSEAEIHTOKATLVCLATGYPDPHVELSWVNGKEVHSGVSTDP 195
Db 1 EDLRNVTTPPKVSLPEPSKAEIANKQKATLVCLARGFPDPHVELSWVNGKEVHSGVSTDP 60

QY 196 QPLKEQPALNDSRYCLSSRLRVSATFWQNPDRNHFRCQVQFGLSENDEWTDRAKPVTOI 255
Db 61 QAYKE---SNYSYCLSSRLRVSATFWHNPDRNHFRCQVQFGLSEEDKWPESGPKPVTON 116

QY 256 VSAEAWGRADCGFTSESYQOGVLSATILYEILGKATLYAVILVSLVLMAMVKKDS 312
Db 117 ISAEAWGRADCGTTSASYHQGVLSATILYEILGKATLYAVILVSLVLMAMVKKNS 173

Search completed: October 11, 2000, 06:09:02
Job time: 51 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 11, 2000, 06:08:11 ; Search time 9.53 Seconds
(without alignments)
1021.047 Million cell updates/sec

Title: US-09-405-940-1

Perfect score: 1664
Sequence: 1 MGTRLLCWAALCLLGADHTG.....AVLSALVLMAMVKRKDSRG 314

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 85661 seqs, 30989116 residues

Total number of hits satisfying chosen parameters: 85661

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	1037	62.3	321	1	TCB_FLV	P11364 feline leuk
2	907	54.5	177	1	TCB_HUMAN	P01850 homo sapien
3	741	44.5	319	1	TCB1_RABIT	P06333 oryctolagus
4	736	44.2	173	1	TCB1_MOUSE	P01852 mus musculus
5	731	43.9	173	1	TCB2_MOUSE	P01851 mus musculus
6	433	26.0	133	1	TVB2_HUMAN	P04435 homo sapien
7	367.5	22.1	134	1	TVB7_MOUSE	P06320 mus musculus
8	337	20.3	135	1	TVB1_HUMAN	P01733 homo sapien
9	249.5	15.0	135	1	TVB1_MOUSE	P01734 mus musculus
10	183	11.0	122	1	TVB5_MOUSE	P04213 mus musculus
11	180.5	10.8	136	1	TVB4_MOUSE	P04212 mus musculus
12	170	10.2	104	1	LAC2_RAT	P20767 rattus norv
13	165	9.9	133	1	TVB2_MOUSE	P01735 mus musculus
14	161.5	9.7	130	1	TVB8_MOUSE	P06321 mus musculus
15	160.5	9.6	213	1	I141_HUMAN	P15814 homo sapien
16	154	9.3	105	1	LAC1_MOUSE	P01843 mus musculus
17	152.5	9.2	105	1	LAC_PIG	P01846 sus scrofa
18	152	9.1	103	1	LAC_CHICK	P20763 gallus gall
19	150	9.0	106	1	KACB_RABIT	P01839 oryctolagus
20	149.5	9.0	391	1	MUCB_HUMAN	P04220 homo sapien
21	149	9.0	104	1	LAC3_MOUSE	P01845 mus musculus
22	147.5	8.9	104	1	LAC1_RAT	P20766 rattus norv
23	146.5	8.8	105	1	LAC_RABIT	P01847 oryctolagus
24	146	8.8	454	1	MUC_HUMAN	P01871 homo sapien
25	144	8.7	458	1	MUC_RABIT	P03988 oryctolagus
26	144	8.7	479	1	MUCM_RABIT	P04221 oryctolagus
27	143	8.6	299	1	ALC_RABIT	P01879 oryctolagus
28	142	8.5	104	1	LAC2_MOUSE	P01844 mus musculus
29	142	8.5	111	1	LV3B_HUMAN	P00748 homo sapien
30	140.5	8.4	104	1	KAC6_RABIT	P03984 oryctolagus
31	140.5	8.4	120	1	TVB3_MOUSE	P01736 mus musculus
32	140	8.4	344	1	ALC_MOUSE	P01878 mus musculus
33	139.5	8.4	105	1	LAC_HUMAN	P01842 homo sapien

34	137.5	8.3	438	HVC2_HETFR
35 <td>137.5 <td>8.2 <td>358 <th>HA1A_MOUSE</th> </td></td></td>	137.5 <td>8.2 <td>358 <th>HA1A_MOUSE</th> </td></td>	8.2 <td>358 <th>HA1A_MOUSE</th> </td>	358 <th>HA1A_MOUSE</th>	HA1A_MOUSE
36 <td>136.5 <td>8.2 <td>421 <th>EPC_MOUSE</th> </td></td></td>	136.5 <td>8.2 <td>421 <th>EPC_MOUSE</th> </td></td>	8.2 <td>421 <th>EPC_MOUSE</th> </td>	421 <th>EPC_MOUSE</th>	EPC_MOUSE
37 <td>135.5 <td>8.1 <td>333 <th>ALC1_HUMAN</th> </td></td></td>	135.5 <td>8.1 <td>333 <th>ALC1_HUMAN</th> </td></td>	8.1 <td>333 <th>ALC1_HUMAN</th> </td>	333 <th>ALC1_HUMAN</th>	ALC1_HUMAN
38 <td>133.5 <td>8.0 <td>353 <th>ALC1_GORGO</th> </td></td></td>	133.5 <td>8.0 <td>353 <th>ALC1_GORGO</th> </td></td>	8.0 <td>353 <th>ALC1_GORGO</th> </td>	353 <th>ALC1_GORGO</th>	ALC1_GORGO
39 <td>133 <td>8.0 <td>340 <th>ALC2_HUMAN</th> </td></td></td>	133 <td>8.0 <td>340 <th>ALC2_HUMAN</th> </td></td>	8.0 <td>340 <th>ALC2_HUMAN</th> </td>	340 <th>ALC2_HUMAN</th>	ALC2_HUMAN
40 <td>132.5 <td>8.0 <td>359 <th>GCAM_MOUSE</th> </td></td></td>	132.5 <td>8.0 <td>359 <th>GCAM_MOUSE</th> </td></td>	8.0 <td>359 <th>GCAM_MOUSE</th> </td>	359 <th>GCAM_MOUSE</th>	GCAM_MOUSE
41 <td>132 <td>7.9 <td>135 <th>TVCL_MOUSE</th> </td></td></td>	132 <td>7.9 <td>135 <th>TVCL_MOUSE</th> </td></td>	7.9 <td>135 <th>TVCL_MOUSE</th> </td>	135 <th>TVCL_MOUSE</th>	TVCL_MOUSE
42 <td>131.5 <td>7.9 <td>288 <th>HA1Y_MOUSE</th> </td></td></td>	131.5 <td>7.9 <td>288 <th>HA1Y_MOUSE</th> </td></td>	7.9 <td>288 <th>HA1Y_MOUSE</th> </td>	288 <th>HA1Y_MOUSE</th>	HA1Y_MOUSE
43 <td>131.5 <td>7.9 <td>365 <th>HA12_MOUSE</th> </td></td></td>	131.5 <td>7.9 <td>365 <th>HA12_MOUSE</th> </td></td>	7.9 <td>365 <th>HA12_MOUSE</th> </td>	365 <th>HA12_MOUSE</th>	HA12_MOUSE
44 <td>131.5 <td>7.9 <td>393 <th>HVC3_HETFR</th> </td></td></td>	131.5 <td>7.9 <td>393 <th>HVC3_HETFR</th> </td></td>	7.9 <td>393 <th>HVC3_HETFR</th> </td>	393 <th>HVC3_HETFR</th>	HVC3_HETFR
45 <td>131 <td>7.9 <td>136 <th>TVC_HUMAN</th> </td></td></td>	131 <td>7.9 <td>136 <th>TVC_HUMAN</th> </td></td>	7.9 <td>136 <th>TVC_HUMAN</th> </td>	136 <th>TVC_HUMAN</th>	TVC_HUMAN

ALIGNMENTS

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RESULT      1
TCB_FLV
ID          TCB_FLV      STANDARD;      PRT;      321 AA.
AC          P11364;
DT          01-JUL-1989 (Rel. 11, Created)
DT          01-JUL-1989 (Rel. 11, Last sequence update)
DT          15-JUL-1989 (Rel. 38, Last annotation update)
DE          T-CELL RECEPTOR BETA CHAIN T17T-22 PRECURSOR.
DE          V-TCR.
GN          Feline leukemia virus.
OC          Viruses; Retrofirdae; Retrovirdae; Mammalian type C retrovirdae.
OS          [1]
RN          SEQUENCE FROM N.A.
RP          MEDLINE; 87144638.
RX          Fulton R., Forrest D., McFarlane R., Onions D., Neil J.C.;
RA          "Retroviral transduction of T-cell antigen receptor beta-chain and
RT          myc genes.";
RL          Nature 326:190-194 (1987).
RN          [2]
RP          REVISION TO 158-159.
RP          Fulton R.;
RA          Submitted (DEC-1987) to the EMBL/GenBank/DBSJ databases.
CC          ---
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CC          or send an email to license@isb-sib.ch).
CC          -----
CC          EMBL; X05155; CAA28801.1;
CC          PIR; C26600; RNMVTC.
CC          PIR; B26600; RNMVTV.
CC          PFAM; PF00047; ig; 2.
CC          T-cell; Receptor; Transmembrane; Glycoprotein; Signal.
CC          SIGNAL
CC          1 28
CC          CHAIN 29 321 T-CELL RECEPTOR BETA CHAIN T17T-22.
CC          DOMAIN 29 122 V SEGMENT.
CC          DOMAIN 123 128 D SEGMENT.
CC          DOMAIN 129 144 J SEGMENT.
CC          DOMAIN 145 321 C REGION.
CC          SEQUENCE 321 AA; 35581 MW; 11D2C3BF56811129 CRC64;
CC          SQ

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	Query Match	62.3%	Score 1037;	DB 1;	Length 321;
	Best Local Similarity	66.1%	Prod. NO. 3.7e-80;		
	Matches 207;	Conservative	Mismatches 78;	Indels	2: Gaps
QY	1	MCETRLCWAALCLLGADHTGAGVTSQPSNKVTEKGDVLRCDPISGHPALYVYRSLGQ	60		
DB	10	MGSRLCCVAICLLGAGPADSLGTQTPRHVYKARGQQVTLSCFPISGHLSLYWQAAVGQ	69		
QY	61	GPEFLYFQGTGAADDSLPNDRFVAVRPGSVSTLIKIQTEGDSAAALVRGAAGWSS	120		
DB	70	GPOLLIOYNEERKGNFP-ERESAOQFPDSHSELNMTSLELTSALYCASSNEQDSE	128		

QY 121 YNEQ-YFGPGRTRVLVLEDKNVPPEVAVFEPSEAEISHTQKATLVCLATGFPDPHVELS 179
 DB 129 YGTFYFEGSRLTVVYEDLKKVSPKVTVPFSEAEISRTKATLVCLATGFPDPHVELS 188
 QY 180 WYNGKEVHSGVSTDPQLKEQPALNDSRYCLSSRLRVSAFWQPNRHFRCQVQFYGLS 239
 DB 189 WYNGKEVHSGVSTDPQLKEQPALNDSRYCLSSRLRVSAFWQPNRHFRCQVQFYGLS 248
 QY 240 ENDEWTDRAKPVTVQTSABEANGRADCGFTSESYQQGVLSATILYEILLGKATLVAVLS 299
 DB 249 KQDWDYPEAKPVTVQTSADTWGRADCGFTSASYQQGVLSATILYEILLGKATLVAVLS 308
 QY 300 ALVLMAMVKRKDS 312
 DB 309 VLALMAKVKRKDS 321

RESULT 2

TCB1_HUMAN
 ID TCB1_HUMAN STANDARD; PRT; 177 AA.
 AC P01850;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE T-CELL RECEPTOR BETA CHAIN C REGION.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A. (CLONE YT35).
 RX MEDLINE; 84142269.
 RA Yanagi Y., Yoshikai Y., Leggett K., Clark S.P., Aleksander I.,
 RA Mak T.W.;
 RT "A human T cell-specific cDNA clone encodes a protein having
 RT extensive homology to immunoglobulin chains.";
 RL Nature 308:145-149(1984).
 DR PIR; A02133; RWHUCY.
 DR PFAM; PF00047; ig: 1.
 KW T-cell; Receptor.
 ET NON_TER 1
 SQ SEQUENCE 177 AA; 19898 MW; 9242AFAA3E3DB4AE CRC64;

Query Match 54.5%; Score 907; DB 1; Length 177;
 Best Local Similarity 97.7%; Pred. No. 1.5e-69;
 Matches 172; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 136 EDLKNVPPEVAVFEPSEAEISHTQKATLVCLATGFPDPHVELSWWNGKEVHSGVSTDP 195
 DB 1 EDLKNVPPEVAVFEPSEAEISHTQKATLVCLATGFPDPHVELSWWNGKEVHSGVSTDP 60
 QY 196 QPLKEQPALNDSRYCLSSRLRVSAFWQPNRHFRCQVQFYGLSENDEWTDRAKPVTVQI 255
 DB 61 QPLKEQPALNDSRYCLSSRLRVSAFWQPNRHFRCQVQFYGLSENDEWTDRAKPVTVQI 120
 QY 256 VSAEANGRADCGFTSESYQQGVLSATILYEILLGKATLVAVLSALVLMAMVKRKD 311
 DB 121 VSAEANGRADCGFTSESYQQGVLSATILYEILLGKATLVAVLSALVLMAMVKRKD 176

RESULT 3

TCB1_RABIT
 ID TCB1_RABIT STANDARD; PRT; 319 AA.
 AC P06333;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DE T-CELL RECEPTOR BETA CHAIN ANA 11.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE; 85242712.
 RA Angiolillo A.L., Lamoyi E., Bernstein K.E., Mage R.G.;
 RT "Identification of genes for the constant region of rabbit T-cell
 RT receptor beta chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4498-4502(1985).
 RN [2].
 RP REVISIONS TO 79-83 AND 104-105.
 RA Mage R.G.;
 RL Submitted (APR-1987) to the PIR data bank.
 DR PIR; A02136; RWRBB.
 DR PFAM; PF00047; ig: 1.
 KW T-cell; Receptor; Transmembrane; Glycoprotein.
 KW DOMAIN 142 273 C REGION.
 FT TRANSMEM 292 313
 FT DOMAIN 314 319 CYTOPLASMIC TAIL.
 FT CARBOHYD 147 147 POTENTIAL.
 FT CARBOHYD 164 164 POTENTIAL.
 FT CARBOHYD 254 254 POTENTIAL.
 FT CARBOHYD 262 262 POTENTIAL.
 SQ SEQUENCE 319 AA; 36068 MW; AAD2C3035ED45306 CRC64;

Query Match 44.5%; Score 741; DB 1; Length 319;
 Best Local Similarity 76.5%; Pred. No. 2.9e-55;
 Matches 140; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
 QY 130 TRLVLEDLKNVPPEVAVFEPSEAEISHTQKATLVCLATGFPDPHVELSWWNGKEVHS 189
 DB 137 TPLHFPEDLANVSAPQVYVDFPSEAEINKTKATLVCLAKDFYDPHVELSWWNGKEVHN 196
 QY 190 GVSTDPQLKEQPALNDSRYCLSSRLRVSAFWQPNRHFRCQVQFYGLSENDEWTDRA 249
 DB 197 GVSTDPQLKEQPALNDSRYCLSSRLRVSAFWQPNRHFRCQVQFYGLSENDEWTDRA 256
 QY 250 KPVTVQTSABEANGRADCGFTSESYQQGVLSATILYEILLGKATLVAVLSALVLMAMVKR 309
 DB 257 KPITQNTSAHTRGRADCGISSASYQQGVLSATLVYEILLGKATLVAVLSALVLMAMVKR 316
 QY 310 KDS 312
 DB 317 KDS 319

RESULT 4

TCB1_MOUSE
 ID TCB1_MOUSE STANDARD; PRT; 173 AA.
 AC P01852;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE T-CELL RECEPTOR BETA-1 CHAIN C REGION.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B10.A;
 RX MEDLINE; 84270704.
 RA Gascolgne N.R.J., Chien Y., Becker D.M., Kavalier J., Davis M.M.;
 RT "Genomic organization and sequence of T-cell receptor beta-chain
 RT constant- and joining-region genes.";
 RL Nature 310:387-391(1984).
 RN [2]
 RP SEQUENCE FROM N.A. (CLONE 86T1).
 RX MEDLINE; 84142271.
 RA Hedrick S.M., Nielsen E.A., Kavalier J., Cohen D.I., Davis M.M.;
 RT "Sequence relationships between putative T-cell receptor polypeptides
 RT and immunoglobulins.";
 RL Nature 308:153-158(1984).
 CC -1- MISCELLANEOUS: REF.2 AUTHORS TRANSLATED THE CODON TAT FOR RESIDUE
 CC 134 AS VAL.
 CC -1- MISCELLANEOUS: CLONE B10.A WAS ISOLATED FROM A CYTOTOXIC T


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CC LYMPOCYTE.
CC -!- MISCELLANEOUS: CLONE 86T1 WAS ISOLATED FROM A CYTOTOXIC T
CC LYMPOCYTE.
DR PIR: A02135; RWSM1C.
DR PFAM: PF00047; Ig; 1.
KW T-cell; Receptor; Transmembrane; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 146 C REGION.
FT TRANSMEM 146 167 POTENTIAL.
FT DOMAIN 168 173 CYTOPLASMIC TAIL.
FT VARIANT 70 70 Y -> H (IN CLONE 86T1).
SQ SEQUENCE 173 AA; 19346 MW; F9B4735E46D3E4D7 CRC64;

Query Match 44.2%; Score 736; DB 1; Length 173;
Best Local Similarity 79.1%; Pred. No. 3.6e-55;
Matches 140; Conservative 16; Mismatches 17; Indels 4; Gaps 1;

QY 136 EDLKNVPPEVAVFPSEAEISHTQKATLVCLATGYDPDHVELSWWVNGKEVHSGVSTDP 195
DB 1 EDLRNVPKVSLEFPSEAEIAKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDP 60
QY 196 OPLKEQPALNDSRYCLSSRLRVSAFWQNPNRHRCQVQFGLSENDEWTDRAKPTQI 255
DB 61 QAYKE-----SNYSYCLSSRLRVSAFWQNPNRHRCQVQFGLSEEDKWPESGPKPTQN 116
QY 256 VSAEAWGRADCGFTSASYOQGVLSATILYEILLGKATLYAVLVSAVLVMAVKKRDS 312
DB 117 ISAEAWGRADCGTTSASVHQVLSATILYEILLGKATLYAVLVGLVMAVKKNS 173

RESULT 5
TCB2_MOUSE STANDARD; PRT; 173 AA.
AC P01851;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE T-CELL RECEPTOR BETA-2 CHAIN C REGION.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B10.A;
RX MEDLINE; 84270704.
RA Gascoigne N.R.J., Chien Y., Becker D.M., Kavalier J., Davis M.M.;
RT "Genomic organization and sequence of T-cell receptor beta-chain
RT constant- and joining-region genes.";
RL Nature 310:387-391(1984).
RN [2]
RP SEQUENCE FROM N.A. (CLONE 2C).
RC STRAIN-BALB.B;
RX MEDLINE; 84245824.
RA Saito H., Kranz D.M., Takagaki Y., Hayday A.C., Eisen H.N.,
RA Tonegawa S.;
RT "Complete primary structure of a heterodimeric T-cell receptor
RT deduced from cDNA sequences.";
RL Nature 309:757-762(1984).
CC -!- MISCELLANEOUS: CLONE B10.A WAS ISOLATED FROM A CYTOTOXIC T
CC LYMPOCYTE.
CC -!- MISCELLANEOUS: CLONE 2C WAS ISOLATED FROM A CYTOTOXIC T
CC LYMPOCYTE.
DR PIR: A02134; RWSMBC.
DR PFAM: PF00047; Ig; 1.
KW T-cell; Receptor; Transmembrane; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 146 C REGION.
FT TRANSMEM 147 168 CYTOPLASMIC TAIL.
FT DOMAIN 169 173
FT VARIANT 50 50 K -> R (IN CLONE 2C).
FT VARIANT 70 70 Y -> H (IN CLONE 2C).
SQ SEQUENCE 173 AA; 19297 MW; A5458149614CF295 CRC64;

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Query Match 43.9%; Score 731; DB 1; Length 173;
Best Local Similarity 78.9%; Pred. No. 9.4e-55;
Matches 139; Conservative 16; Mismatches 18; Indels 4; Gaps 1;

QY 136 EDLKNVPPEVAVFPSEAEISHTQKATLVCLATGYDPDHVELSWWVNGKEVHSGVSTDP 195
DB 1 EDLRNVPKVSLEFPSEAEIAKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDP 60
QY 196 OPLKEQPALNDSRYCLSSRLRVSAFWQNPNRHRCQVQFGLSENDEWTDRAKPTQI 255
DB 61 QAYKE-----SNYSYCLSSRLRVSAFWQNPNRHRCQVQFGLSEEDKWPESGPKPTQN 116
QY 256 VSAEAWGRADCGFTSASYOQGVLSATILYEILLGKATLYAVLVSAVLVMAVKKRDS 312
DB 117 ISAEAWGRADCGTTSASVHQVLSATILYEILLGKATLYAVLVGLVMAVKKNS 173

RESULT 6
TVB2_HUMAN STANDARD; PRT; 133 AA.
AC P04435;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE T-CELL RECEPTOR BETA CHAIN V REGION CTL-L17 PRECURSOR.
GN TCRB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86276770.
RA Leiden J.M., Fraser J.D., Strominger J.L.;
RT "The complete primary structure of the T-cell receptor genes from an
RT alloreactive cytotoxic human T-lymphocyte clone.";
RL Immunogenetics 24:17-23(1986).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS DERIVED FROM A HUMAN CYTOTOXIC
CC T-LYMPOCYTE THAT IS T3+, T4+, T8+.
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CC -----
DR EMBL; M15564; AAA61027.1; -.
DR PIR; A02001; RWHU7B.
DR PFAM; PF00047; Ig; 1.
KW T-cell; Receptor; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 133 T-CELL RECEPTOR BETA CHAIN V REGION CTL-
FT L17.
FT DOMAIN 22 114 V SEGMENT.
FT DOMAIN 115 118 D SEGMENT.
FT DOMAIN 119 133 J SEGMENT.
FT CARBOHYD 30 30
FT CARBOHYD 37 37
FT DISULFID 42 111
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14999 MW; 21030818D18D341F CRC64;

Query Match 26.0%; Score 433; DB 1; Length 133;
Best Local Similarity 62.2%; Pred. No. 7.9e-30;
Matches 84; Conservative 15; Mismatches 34; Indels 2; Gaps 1;

QY 1 MGTSLCWALCLLGADHTGACVSTPSNKVTEKGDKVELRCDPTSGHTALYVYRQSLGQ 60
DB 1 MGTSLCWALCLLGADHTGCVSQNPNTTKRGQNTFRCDPTSEHRLYVTRQLGQ 60

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]

DR PFAM; PF00047; ig; 1.

RN [1]

```
KW T-cell; Receptor; Signal.
FT SIGNAL 1 20
FT CHAIN 21 - 135
FT T-CELL RECEPTOR BETA CHAIN V REGION
FT 3H.25.
FT DOMAIN 21 115
FT V SEGMENT.
FT DOMAIN 116 118
FT D SEGMENT.
FT DOMAIN 119 135
FT J SEGMENT.
FT DISULFID 42 111
FT BY SIMILARITY.
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15123 MW; C0FF1DDACF37E76D CRC64;

Query Match 15.0%; Score 249.5; DB 1; Length 135;
Best Local Similarity 42.2%; Pred. No. 2.2e-14;
Matches 57; Conservative 16; Mismatches 59; Indels 3; Gaps 1;

QY 1 MGRLLCWAALCLLGADHTGAGSOTPSNKVTEKGDVELRCDPISGHTALYWRQS 60
Db 1 MATRLCYTVLCGLARILNSKVQPRVLYKGGQKAKMRCIPEKGHVVFVYQKNKN 60

QY 61 GPPELLYFQGTGAADSGPLNDRFFAVRPEGSVSTLKIQRTQGGDSAAAYLRAGVAGWSS 120
Db 61 EFRLINQVQVQIDMTKRFSAECPNSPCSLIQSSAGDSALYLCASSLFGTSD 120

QY 121 YNEQYFGPGTRLTVL 135
Db 121 YT---FGSGTRLVLI 132

RESULT 10
TVB4_MOUSE STANDARD; PRT; 122 AA.
AC P04213;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE T-CELL RECEPTOR BETA CHAIN V REGION C5 PRECURSOR (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85036636.
RA Patten P., Yokota T., Rothbard J., Chien Y., Arai K., Davis M.M.;
RT "Structure, expression and divergence of T-cell receptor beta-chain
variable regions.";
RL Nature 312:40-46(1984).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS DERIVED FROM A T-HELPER CLONE.
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CC -----
CC EMBL; X01643; CAA25800.1; -
CC PIR; A02007; RWSLB.
CC PFAM; PF00047; Ig; 1.
CC T-cell; Receptor; Signal.
KW SIGNAL 1 21
FT CHAIN 22 136
FT DOMAIN 22 116
FT V SEGMENT.
FT DOMAIN 117 120
FT D SEGMENT.
FT DOMAIN 121 136
FT J SEGMENT.
FT DISULFID 45 113
FT BY SIMILARITY.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15369 MW; F74DCC0414088D02 CRC64;

Query Match 10.8%; Score 180.5; DB 1; Length 136;
Best Local Similarity 32.6%; Pred. No. 1.4e-08;
Matches 45; Conservative 25; Mismatches 63; Indels 5; Gaps 3;

QY 1 MGRLLCWAALCLLGADHT---GAGVSQTPSNKVTGKGDVELRCDPISGHTALYWRQS 57
Db 1 MNKWVFCWVTLCLLAVETHGDSGIIQTPEFLIQEGQKLTLCQQNFNDHTMYWRQD 60

QY 58 LCGQPEFLIYFQGTGAADSGPLNDRFFAVRPEGSVSTLKIQRTQGGDSAAAYLRAGVAG 117
Db 61 SGKGLR-LIYYSITENDLQKGLDSEGYDASREKKSFSILTVTSQKNMTVFLCAS-SIR 118

QY 118 WSSYNEQYFGPGTRLTVL 135
Db 119 LASAETLYFGSGTRLTVL 136

RESULT 12
LAC2_RAT STANDARD; PRT; 104 AA.
ID LAC2_RAT
AC P20767;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG LAMBDA-2 CHAIN C REGION.
```

```

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE: 87305594.
RA Steen M.L., Hellman L., Pettersson U.;
RT "The immunoglobulin lambda locus in rat consists of two C lambda
RL genes and a single v lambda gene.";
RL Gene 55:75-84(1987).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC -----
DR EMBL; M22521; AAA1420.1; ALT_INIT.
DR PIR; B27390; B27390.
DR PFAM; PF00047; ig; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 27 85
FT DISULFID 103 103
FT SEQUENCE 104 AA; 11318 MW; F087906DE43F7276 CRC64;
SQ -----

Query Match 10.2%; Score 170; DB 1; Length 104;
Best Local Similarity 41.5%; Pred. No. 7.8e-08;
Matches 39; Conservative 12; Mismatches 35; Indels 8; Gaps 3;

QY 144 PEVAVFPEPSAEISHTQKATLVCLATGFYDPHVLSWVNGKEVHSGVSDPQPLKEQPA 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 PTLTVFPSPSTEL-QGNKATLVCLISDFPSDEVANKANGAPISQGVDT-----ANPT 58

QY 204 LNSRVCLSRLVSAFTWQNPNNHFCQVQFYG 237
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 KQGNKYIASSFLRTAQWRS-RNSFFCQVTHEG 91

RESULT 13
TVB2_MOUSE
ID TVB2_MOUSE STANDARD; PRT; 133 AA.
AC P01735;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE T-CELL RECEPTOR BETA CHAIN V REGION 86T1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RX SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RX MEDLINE: 84142271.
RA Hedrick S.M., Nielsen E.A., Kaveler J., Cohen D.I., Davis M.M.;
RT "Sequence relationships between putative T-cell receptor polypeptides
RT and immunoglobulins.";
RL Nature 308:153-158(1984).
DR PIR; A02004; RWMVS8.
DR PFAM; PF00047; ig; 1.
DR T-cell; Receptor; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 133
FT DOMAIN 22 133
FT DOMAIN 114 133
FT CARBOHYD 36 36
FT CARBOHYD 75 75
FT DISULFID 41 109
FT NON_TER 133 133
BY SIMILARITY.
T-CELL RECEPTOR BETA CHAIN V REGION 86T1.
V SEGMENT.
J SEGMENT.

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Search completed: October 11, 2000, 06:09:24
Job time: 73 sec

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AC BL5814;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR.
GN IGL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RX MEDLINE; 89315835.
RA Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
RA McKearn J.P.;
RT "Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are
RT expressed in pre-B cells and may encode the human immunoglobulin
RT omega light-chain protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5552-5556(1989).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=LYMPHOID;
RC MEDLINE; 91108327.
RX Evans R.J., Hollis G.F.;
RA "Genomic structure of the human Ig lambda 1 gene suggests that it may
RT be expressed as an Ig lambda 14.1-like protein or as a canonical B
RT cell Ig lambda light chain: implications for Ig lambda gene
RT evolution.";
RL J. Exp. Med. 173:305-311(1991).
CC -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN PRE-B-CELLS AND A SPECIAL
CC B-CELL LINE (WHICH IS SURFACE IG NEGATIVE).
CC -!- MISCELLANEOUS: THIS LAMBDA LIGHT-CHAIN-RELATED PROTEIN MAY BE THE
CC IMMUNOGLOBULIN OMEGA LIGHT-CHAIN.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SHOWS
CC SIMILARITY TO LAMBDA LIGHT CHAIN IN C-TERMINAL HALF (J AND C
CC REGIONS).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M27749; AAA36100.1; -.
DR EMBL; M34513; AAA36096.1; -.
DR EMBL; M34511; AAA36096.1; JOINED.
DR EMBL; M34512; AAA36096.1; JOINED.
DR F01; A33911; A33911.
DR HSSP; P01842; 7FAB.
DR PFAM; PF00047; ig; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; B-cell; Signal.
FT SIGNAL 1 ?
FT CHAIN 2 213 IMMUNOGLOBULIN-RELATED 14.1 PROTEIN.
FT DOMAIN 97 108 J REGION (BY SIMILARITY TO LAMBDA
FT LIGHT-CHAIN).
FT DOMAIN 109 213 C REGION (BY SIMILARITY TO LAMBDA
FT LIGHT-CHAIN).
FT SEQUENCE 213 AA; 22963 MW; 9133A7742B943C79 CRC64;
SQ
Query Match 9.6%; Score 160.5; DB 1; Length 213;
Best local similarity 36.6%; Pred. No. 1.2e-06;
Matches 41; Conservative 18; Mismatches 44; Indels 9; Gaps 5;
QY 126 FGGPTRLTVLEDKNVPPEVPEPSEARISHTOKATVCLATGYPDPHVELSWVNGK 185
DB 98 FGGSTQTLTVLSQPKAT--PSVTLPFSSSEL-QANKATVCLMNDYFGILITWKADGT 154
QY 186 EVHSGVSTDPQPLKEQPALNDSYCLSSRLRSVATFWMQNRNHRFCQVQFYG 237
DB 155 PITQGVEM-TTPSKQ----SNKYAASSVLSLTPEQWRS-RRSYSCQVMHEG 200
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 11, 2000, 06:08:41 ; Search time 18.52 Seconds
(without alignments)
1583.125 Million cell updates/sec

Title: US-09-405-940-1
Perfect score: 1664
Sequence: 1 MGRLLCWAALCLLGADHTG.....AVLYSAEVLAMVKRDSRG 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_14:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	181	10.9	214	11 Q9RIA5	Q9RIA5 mus musculu
2	177.5	10.7	259	13 Q90530	Q90530 ginglymosto
3	166	10.0	268	13 Q90524	Q90524 ginglymosto
4	165.5	9.9	267	13 Q90529	Q90529 ginglymosto
5	161	9.7	257	13 Q90536	Q90536 ginglymosto
6	156.5	9.4	437	11 Q9RIA4	Q9RIA4 mus musculu
7	155.5	9.3	252	13 Q90568	Q90568 ginglymosto
8	154	9.3	684	13 Q90544	Q90544 ginglymosto
9	146.5	8.8	509	11 Q90907	Q90907 mus musculu
10	145.5	8.7	137	4 Q9UDR1	Q9UDR1 homo sapien
11	145.5	8.7	333	7 Q31522	Q31522 poecilia re
12	145.5	8.7	509	11 Q9WTN4	Q9WTN4 mus musculu
13	145	8.7	345	7 P79599	P79599 rattus norv
14	142.5	8.6	361	7 P79599	P79599 rattus norv
15	142	8.5	348	7 O46875	O46875 ratallurus p
16	141.5	8.5	237	13 Q90545	Q90545 ginglymosto
17	141.5	8.5	346	7 P78088	P78088 rattus norv
18	141.5	8.5	367	7 P79589	P79589 rattus norv
19	141	8.5	296	7 Q31274	Q31274 rattus norv

20	141	8.5	346	11 Q9QXQ3	Q9QXQ3 rattus norv
21	141	8.5	347	7 Q31257	Q31257 rattus norv
22	141	8.5	360	7 Q31266	Q31266 rattus norv
23	141	8.5	370	7 Q31258	Q31258 rattus norv
24	141	8.5	380	7 Q19446	Q19446 rattus norv
25	140.5	8.4	346	7 Q95459	Q95459 rattus norv
26	137	8.2	365	11 Q61892	Q61892 mus musculu
27	136	8.2	366	7 P79587	P79587 rattus norv
28	135.5	8.1	384	4 Q9UP60	Q9UP60 homo sapien
29	135.5	8.1	509	11 Q9QX57	Q9QX57 mus musculu
30	135.5	8.1	513	11 P97797	P97797 mus musculu
31	134.5	8.1	362	7 Q95557	Q95557 peromyscus
32	134.5	8.1	368	11 Q64272	Q64272 mus musculu
33	134	8.1	345	7 Q95565	Q95565 rattus norv
34	134	8.1	345	11 Q9QXQ1	Q9QXQ1 rattus norv
35	134	8.1	346	11 Q9QXP8	Q9QXP8 rattus norv
36	134	8.1	365	7 Q31149	Q31149 mus musculu
37	133	8.0	367	7 Q31254	Q31254 rattus norv
38	132.5	8.0	122	4 Q99603	Q99603 homo sapien
39	132.5	8.0	122	4 Q99604	Q99604 homo sapien
40	132.5	8.0	365	7 Q31188	Q31188 mus musculu
41	132.5	8.0	368	11 Q61642	Q61642 mus musculu
42	132	7.9	188	7 Q31593	Q31593 salmo salar
43	132	7.9	506	6 Q46632	Q46632 bos taurus
44	130.5	7.8	368	7 Q61896	Q61896 mus musculu
45	130	7.8	179	7 Q31272	Q31272 rattus norv

ALIGNMENTS

RESULT 1
Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5;
DI 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DI KAPPA LIGHT-CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Mistra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv)".
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR INTERPRO; IPR000495; -.
DR PFM; PF00047; ig. 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match	10.9%;	Score 181;	DB 11;	Length 214;
Best Local Similarity	25.9%;	Pred No. 2,8e-09;		
Matches	60;	Conservative	40;	Mismatches 70;
Indels	52;	Gaps	12;	
QY	23	VSQTSNKVTEKGVKDELRCDFISG-HTALYWRSLQGGPEFLIY-----FQ 69		
Db	4	LTQSPSSMYASLGERTVITCKASQDINSYLSFWFQKPGKSPKTLIYRANRLVDGVPSRFS 63		
QY	70	GTCGAADSLPNDRFVAFVPEGSVSTLKTQTEQDSRAYLRAGVAGWSYNEY---- 125		
Db	64	GGSGQDQSVL-----TISL-----EYEDMGII-----YCLQYDFEP 95		
QY	126	--FGPGTRITVLLEDLKNV--FPPEVAVFPPESEAIHSHTOKATIVLCATGFPDHWELSWWV 182		

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db      96  FTGSGTKL----EIKRAADAAPTIVSFPSPSEQLT-SGGASVVCFLNNFYPKDINVAWKI 150
QY      183  NGKEVHSGV--STDQPLKEQPALNDSRYCLSLRVASATFWQNPRNHFRQ 232
db      151  DGSERQNGVSWTDQDSK-----DSTVSMSTLTLLTKDEYER-HNSYTC 195

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RESULT 2

Q90530	PRELIMINARY;	PRT;	259 AA.
ID	Q90530		
AC	Q90530;		
DT	01-NOV-1996 (TREMblrel. 01, Created)		
DT	01-NOV-1996 (TREMblrel. 01, Last annotation update)		
DT	01-MAY-2000 (TREMblrel. 13, Last annotation update)		
DE	NOVEL ANTIGEN RECEPTOR (FRAGMENT).		
OS	Ginglymostoma cirratum (Nurse Shark).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;		
OC	Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;		
OC	Orectolobiformes; Ginglymostomatidae; Ginglymostoma.		
RN	[1]		
	SEQUENCE OF 1-235 FROM N.A.		
RC	TISSUE-SPLEEN;		
RC	MEDLINE: 95183140.		
RA	Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,		
RA	Flajnik M.F.;		
RT	"A new antigen receptor gene family that undergoes rearrangement and		
RT	extensive somatic diversification in sharks."		
RL	Nature 374:168-173(1995).		

RESULT	3	
ID	Q90524	
AC	Q90524;	PRELIMINARY;
DT	01-NOV-1996	(TREMblrel. 01, Created)
DT	01-NOV-1996	(TREMblrel. 01, Last sequence update)
DT	01-MAY-2000	(TREMblrel. 13, Last annotation update)
DE	DE NOVEL ANTIGEN RECEPTOR (FRAGMENT).	
OS	Ginglymstoma cirratum (Nurse shark).	

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 CC Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
 CC Orectolobiformes; Ginglymostomatidae; Ginglymostoma.
 [1]
 RN SEQUENCE OF 1-240 FROM N.A.
 RP
 RP TISSUE=SPLEEN;
 RC
 RC MEDLINE: 95183140.
 RA Greenberg A.S.; Avila D., Hughes M., Hughes A., McKinney E.C.,
 RA Flajnik M.F.;
 RA "A new antigen receptor gene family that undergoes rearrangement and
 RT extensive somatic diversification in sharks.",
 RT Nature 374:168-173(1995).
 RT

```

RESULT      4
Q90529      PRELIMINARY:      PRT;      267 AA.
AC Q90529;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE NOVEL ANTIGEN RECEPTOR (FRAGMENT).
OS Ginglymstoma cirratum (Nurse shark).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
OC Orectoibiformes; Ginglymstomatidae; Ginglymstoma.
[1]
RN SEQUENCE OF 1-243 FROM N.A.
RP TISSUE=SPLEEN;
RX MEDLINE: 95183140.
RA Greenberg A.S., Avila D., Hughes M., Hughes E.C.,
RA Flajnik M.F.;
RT "A new antigen receptor gene family that undergoes rearrangement and
RT extensive somatic diversification in sharks.";
RL Nature 374:168-173(1995).

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RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=SPLEEN;
RA      Greenberg A.S.;
RL      Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U18686; AAB48357.1; -.
DR      HSSP; P01842; 7FAB.
DR      INTERPRO; IPR000495; -.
DR      INTERPRO; IPR003006; -.
DR      PFAM; PF00047; Ig; 2.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT      NON_TER 267
SQ      SEQUENCE 267 AA; 29402 MW; 0E1362456E22CB94 CRC64;

Query Match          9.9%; Score 165.5; DB 13; Length 267;
Best Local Similarity 26.9%; Pred. No. 1.1e-07;
Matches 63; Conservative 36; Mismatches 100; Indels 35; Gaps

QY 23 VSQTPSNKVKTEKGDVLRCLRC---DPISGHTALYWRQSLGQGPFLIYFQGTGAADDSGL 79
Db 21 VDQTPHSITKETGESLTINCVRDSACGLSNAQWYRERSGSTKEENI-SQARYVE--- 75
QY 80 PNDRFFAVRPEGSVSLKIQRTQEGDSAAAYLRAGVAAGW-----SSYNEQY--FG 127
Db 76 -----TVNRESKFSRLINDLTVEDSGSY--RCMASTWYTDIEGGEIGTGPCNRQHDVYG 127
QY 128 PGRLTVLEDLKNVPEPPEVAVFPEPSEAEISHTQKATLVCLATGYDPDHVELSWWVANGKEV 187
Db 128 ADTWTVTNPGIP-LSPPIVLSLLHSATEEQRANFVQLVCLISGYYPENTAVSQKTKTII 186
QY 188 HSGVSTDPQLKEQPALNDSRYCLSSRLRVSAFTWQNPNRHFRQCQVQFVGLSEN 241
Db 187 TSGFAT-TSPVK--TSSND--FSCASLLKVPLOEWSR-GSVYSCQVSHSATSSN 234

RESULT 5
QY0536 PRELIMINARY; PRT; 257 AA.
AC QY0536;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMELrel. 14, Last annotation update)
DE NOVEL ANTIGEN RECEPTOR (FRAGMENT).
OS Ginglymostoma cirratum (Nurse shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
OC Orectolobiformes; Ginglymostomatidae; Ginglymostoma.
RN [1]
RP SEQUENCE OF 1-242 FROM N.A.
RC TISSUE=SPLEEN;
RX MEDLINE; 95183140.
RA Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
RA Flajnik M.F.;
RT "A new antigen receptor gene family that undergoes rearrangement and
RT extensive somatic diversification in sharks.";
RL Nature 374:168-173(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Greenberg A.S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U18693; AAB48364.1; -.
DR      HSSP; P01842; 7FAB.
DR      INTERPRO; IPR000495; -.
DR      INTERPRO; IPR003006; -.
DR      PFAM; PF00047; Ig; 2.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT      NON_TER 257
SQ      SEQUENCE 257 AA; 28083 MW; BAD019A99D0BC491 CRC64;

Query Match          9.7%; Score 161; DB 13; Length 257;
Best Local Similarity 27.1%; Pred. No. 1.5e-06;
Matches 58; Conservative 33; Mismatches 98; Indels 25; Gaps

QY 25 QTPSNKVKTEKGDVLRCLRCDPISGHT---ALYWRQSLGQGPFLIYFQGTGAADDSGLP 80
Db 4 QESGGGLVAPGGSLKLS-C-AASGFTFSSYAMSVWRQTPKRLWVASFSSGGIIYYTDSV 62
QY 81 NDREFFAVR-PEGSVSLKIQRTQEGDSAAAYLRAGVAAGWSSYNEQYFGPCTRLTVLEDLK 139
Db 63 KGRFTYKDKRNIUSLQSSLSRSEDAMYCAR-----GDYS-AYWGGTTLVTV--SAA 114
QY 140 NVFPEPPEVAFPEPSEAEISHTQKATLVCLATGYDPDHVELSWWVANGKEVSGYSTDPQLK 199
Db 115 KITPPSVYPLAPGSAQAQTNM-VTLGLCVKGYFPEPVTW--NSGSLSSGVHTFP---- 167
QY 200 EQPALNDSRYCLSSRLRVSAFTWQNPNRHFRQCV 233
Db 168 --AVLQSDLYTLSSSVTFPSTW--PSETVTCNV 197

RESULT 7
QY0568 PRELIMINARY; PRT; 252 AA.
ID QY0568
AC QY0568;

Query Match          9.4%; Score 156.5; DB 11; Length 437;
Best Local Similarity 27.1%; Pred. No. 1.5e-06;
Matches 58; Conservative 33; Mismatches 98; Indels 25; Gaps

QY 25 QTPSNKVKTEKGDVLRCLRCDPISGHT---ALYWRQSLGQGPFLIYFQGTGAADDSGLP 80
Db 4 QESGGGLVAPGGSLKLS-C-AASGFTFSSYAMSVWRQTPKRLWVASFSSGGIIYYTDSV 62
QY 81 NDREFFAVR-PEGSVSLKIQRTQEGDSAAAYLRAGVAAGWSSYNEQYFGPCTRLTVLEDLK 139
Db 63 KGRFTYKDKRNIUSLQSSLSRSEDAMYCAR-----GDYS-AYWGGTTLVTV--SAA 114
QY 140 NVFPEPPEVAFPEPSEAEISHTQKATLVCLATGYDPDHVELSWWVANGKEVSGYSTDPQLK 199
Db 115 KITPPSVYPLAPGSAQAQTNM-VTLGLCVKGYFPEPVTW--NSGSLSSGVHTFP---- 167
QY 200 EQPALNDSRYCLSSRLRVSAFTWQNPNRHFRQCV 233
Db 168 --AVLQSDLYTLSSSVTFPSTW--PSETVTCNV 197

RESULT 6
QY0568 PRELIMINARY; PRT; 437 AA.
ID QY0568;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMELrel. 14, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF152372; AAD40243.1; -.
DR      INTERPRO; IPR000495; -.
DR      INTERPRO; IPR003006; -.
DR      PFAM; PF00047; Ig; 4.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT      NON_TER 437
FT      NON_TER 437
SQ      SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match          9.4%; Score 156.5; DB 11; Length 437;
Best Local Similarity 27.1%; Pred. No. 1.5e-06;
Matches 58; Conservative 33; Mismatches 98; Indels 25; Gaps

QY 25 QTPSNKVKTEKGDVLRCLRCDPISGHT---ALYWRQSLGQGPFLIYFQGTGAADDSGLP 80
Db 4 QESGGGLVAPGGSLKLS-C-AASGFTFSSYAMSVWRQTPKRLWVASFSSGGIIYYTDSV 62
QY 81 NDREFFAVR-PEGSVSLKIQRTQEGDSAAAYLRAGVAAGWSSYNEQYFGPCTRLTVLEDLK 139
Db 63 KGRFTYKDKRNIUSLQSSLSRSEDAMYCAR-----GDYS-AYWGGTTLVTV--SAA 114
QY 140 NVFPEPPEVAFPEPSEAEISHTQKATLVCLATGYDPDHVELSWWVANGKEVSGYSTDPQLK 199
Db 115 KITPPSVYPLAPGSAQAQTNM-VTLGLCVKGYFPEPVTW--NSGSLSSGVHTFP---- 167
QY 200 EQPALNDSRYCLSSRLRVSAFTWQNPNRHFRQCV 233
Db 168 --AVLQSDLYTLSSSVTFPSTW--PSETVTCNV 197

RESULT 7
QY0568 PRELIMINARY; PRT; 252 AA.
ID QY0568
AC QY0568;
```

DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE NOVEL ANTIGEN RECEPTOR (FRAGMENT).
 OS Ginglymostoma cirratum (Nurse shark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
 OC Orectolobiformes; Ginglymostomatidae; Ginglymostoma.
 RN [1]
 RP SEQUENCE OF 1-239 FROM N.A.
 RC TISSUE=SPLEEN;
 RX MEDLINE; 95183140.
 RA Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
 RA Flajnik M.F.,
 RA "A new antigen receptor gene family that undergoes rearrangement and
 RT extensive somatic diversification in sharks."
 RL Nature 374:168-173(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN;
 RA Greenberg A.S.,
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U18725; AB42387.1; -.
 DR HSSP; P01842; 7FAB.
 DR INTERPRO; IPR000495; -.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; ig; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 FT NON_TER 252 252
 SQ SEQUENCE 252 AA; 27356 MW; 117F2225B2E17EDF CRC64;

Query Match 9.3%; Score 155.5; DB 13; Length 252;
 Best Local Similarity 27.6%; Pred. No. 8.6e-07;
 Matches 64; Conservative 31; Mismatches 102; Indels 35; Gaps 11;

QY 23 VSQTPSNKYTEKGDVLRCDPISGHTALYWRQSLGQGPFLI----YFQGTGAADSG 78
 DB 21 VLQTPSAVTKETGSLTINC-----VLRDSPQSLAGTCWYFTRSGSRSEER 66
 QY 79 L-PNDRFFAVRPEGSVS-TLKIQTQEGDGAAYLRAGVAAGWS-----YNEQVFGPG 129
 DB 67 IRAGRVVETVNSGSKSFSLKINDLTVEDGGTY-RCVAGTHSGCALCSFQIEATCGEG 125
 QY 130 TRLVLEDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFPYDPHVELSWYNGKEVHS 189
 DB 126 TAVTVNPGIP-PSPIIVSLLSHSATEEQANRFVOLVCLISGYYPENIAVSWQNTKTITS 184
 QY 190 GVSTDPOPLKEQPALNDSRYCLSLRLVSATFWQNPENHFRFCOVQVGLSEN 241
 DB 185 GFAT-TSPVK--TSSND--FSCASLHKVPLQEWNR-GSVYSCQVSHSATSSN 230

RESULT 8
 ID Q90544 PRELIMINARY; PRT; 684 AA.
 AC Q90544;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE NOVEL ANTIGEN RECEPTOR PRECURSOR.
 OS Ginglymostoma cirratum (Nurse shark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
 OC Orectolobiformes; Ginglymostomatidae; Ginglymostoma.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN;
 RX MEDLINE; 95183140.
 RA Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
 RA Flajnik M.F.,
 RA "A new antigen receptor gene family that undergoes rearrangement and
 RT extensive somatic diversification in sharks."

RL Nature 374:168-173(1995).
 DR EMBL; U18701; AB48195.1; -.
 DR INTERPRO; IPR000495; -.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; ig; 6.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 684 NOVEL ANTIGEN RECEPTOR.
 SQ SEQUENCE 684 AA; 75224 MW; 2FF9D2071CDA6DFD CRC64;
 Query Match 9.3%; Score 154; DB 13; Length 684;
 Best Local Similarity 22.8%; Pred. No. 4.7e-06;
 Matches 64; Conservative 41; Mismatches 110; Indels 56; Gaps 12;
 QY 23 VSQTPSNKYTEKGDVLRCDPISGHTALYWRQSLGQGPFLIYFQGTGAAD 75
 DB 21 VDQTPRSVAKAEQVLTINCVLRGANYELAKGSTC-WYRKKS-----SKVE 66
 QY 76 DSCLPNDRFFAVRPEGSVS-TLKIQTQEGDGAAYLRAGVAAGWSYNEQYF----- 126
 DB 67 ESITKGRVETVNSGSKSFSLRINDLTIEDAGDYR---CAANEAAADCMFVGCTIYPF 122
 QY 127 ----GPGTRLTVLEDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFPYDPHVELSWV 182
 DB 123 SGAGSGSTAVTTPGIP-PSPIIVSLLSHSATEEQANRFVOLVCLISGYYPENIAVSWQ 181
 QY 183 NGEVHSGVSTDPQLKEQPALNDSRYCLSLRLVSATFWQNPENHFRFCOVQVGLSEND 242
 DB 182 NTKTITSGFAT-TSPVK--TSSND--FSCASLHKVPLQEWNR-GSVYSCQVSHSATSSN 235
 QY 243 E-----WTQDRAPKPTQIVSAPAWG 262
 DB 236 RKEIRSTSEIALLRDPVTVEEIWIDKSLTICEVLSVTSAG 276

RESULT 9
 ID O08907 PRELIMINARY; PRT; 509 AA.
 AC O08907;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE BRAIN IMMUNOLOGICAL-LIKE PROTEIN (BIT).
 GN BIT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=BRAIN;
 RX MEDLINE; 97230468.
 RA Ohnishi H., Kubota M., Sano S.;
 RT "BIT (Bit) maps to mouse chromosome 2."
 RL Genomics 40:504-506(1997).
 DR EMBL; D85785; BAA20376.1; -.
 DR MGI; MGI:107947; Bit.
 DR INTERPRO; IPR000495; -.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; ig; 3.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 SQ SEQUENCE 509 AA; 56033 MW; 1E377ACEC31BA13E CRC64;

Query Match 8.8%; Score 146.5; DB 11; Length 509;
 Best Local Similarity 22.4%; Pred. No. 1.6e-05;
 Matches 95; Conservative 58; Mismatches 132; Indels 139; Gaps 24;
 QY 1 MGTRELIC--WAALCL-LGADHTGAGVSQTPSNKYTEKGDVLRCD----PISGHTALY 52
 DB 11 LGPLLLLLLSASCFTGATGTGTEVKVTPPEKSVSVAAGDSTILNCTVTSLLPVG---PIR 67

```
QY 53 WYRQSLGQGPPEFLIYFQGTGA-----ADDSGLPNDRFFAVR-----PE--GSVSTLKI 98
Db 68 WYR---GVQSRLLIYFSGTGEHFPVRNVSDTKRNNMDFSIRISNVPEADAGTICYKVF 124
QY 99 QR--TEQDGAAYLRACVAAGSSYNEQYFGPGTGLTLVLEDIKNVFPPEVAVPEPSEAEIS 157
Db 125 QRGSSSEPD-----EQSGGGTEYVV---LAKPSPEVS--GPADRGTP 163
QY 158 HTQKATLVCLATGFFPDHVELSWVNGKEVH-----SG-----VSTDPOPLKEQPA 203
Db 164 -DQVNFCTKSHGFSRNTLTKWFKDQGLHPLFTVNFSGKNVSYNISSTVRVVLNSMD 222
QY 204 LNSRYC-----LSSRLRVSAT--FWQNP-----RNHFRQC----- 232
Db 223 VNSKVCCEVAHITLDRSPGLRGIANLSNFIRVSTFKVTOQPTSMNQVNLICRAERFYPE 282
QY 233 -VOFYGLSENDEWTDQRAKPVTO-----IVSAEANGRADCGFT----- 269
Db 283 DLQLIWLENGVSRNDTPKNLTKNTDGTNYTSLFLVNSSA-HREDVVFTQCVKHDQQPA 341
QY 270 -----SESYOQGVL-----SATLYEILIG---KATLYAVLYSALVLMAMVKRK 310
Db 342 ITRNHVVLGLAHSSDQGSQCTPFGNNATHNWNVFIGVACALLVVLLMAALYLIRIKQK 401
QY 311 DSRG 314
Db 402 KAKG 405

RESULT 10
Q9UDR1
ID Q9UDR1 PRELIMINARY; PRT; 137 AA.
AC Q9UDR1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE T-CELL RECEPTOR GAMMA CHAIN, TRGV9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99063792.
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Arnett C., Wohlmann P., Le T.;
RT "The sequence of Homo sapiens BAC clone RP11-121A8.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006033; RAD15557.1;
DR INTERPRO; IPR003006;
DR PFAM; PF00047; ig; 1.
KW Receptor.
SQ SEQUENCE 137 AA; 15184 MW; B1F09F63D3671609 CRC64;
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Query Match 8.7%; Score 145.5; DB 4; Length 137;
Best Local Similarity 33.3%; Pred. No. 3.2e-06;
Matches 44; Conservative 19; Mismatches 59; Indels 17; Gaps 7;

```
QY 10 ALCLLGADHTGAGVSQTPSKVTEKGDVLRCDPIFG-----HTALYWRQSLGQGPFL 65
Db 15 ALCVYGAGH----LEQPOISSTKTLKRTARLEC-VVSGITISATSVYWRERPEGVIOFL 69
```

```
QY 66 --IYFQGTGAADDSGLPNDRFFAVR--PEGSVSTLKIQTQEQDGAAYLRAGVAAGWSYN 122
Db 70 VSIISYDGT-VKESGIPSGKEVDRIPTSTLTIIHNVKEQDIATY----YCALWEVHS 124
QY 123 EYFQGPGLTLV 134
Db 125 SRQEPESHINW 136

RESULT 11
Q31522
ID Q31522 PRELIMINARY; PRT; 333 AA.
AC Q31522
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE MHC CLASS IA (FRAGMENT).
OS Poecilia reticulata (Guppy).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Acanthopterygii;
OC Atherinomorpha; Cyprinodontiformes; Cyprinodontidae; Poeciliidae;
OC Poecilia.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96128251.
RA Sato A., Figueroa F., O'Huigin C., Reznick D.N., Klein J.;
RT "Identification of major histocompatibility complex genes in the
RT guppy, Poecilia reticulata.";
RL Immunogenetics 43:38-49(1996).
DR EMBL; Z54085; CAA90791.1;
DR INTERPRO; IPR001039;
DR INTERPRO; IPR003006;
DR PFAM; PF00047; ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
SQ SEQUENCE 333 AA; 37165 MW; D9C042B504B8014D CRC64;
```

Query Match 8.7%; Score 145.5; DB 7; Length 333;
Best Local Similarity 22.1%; Pred. No. 1.1e-05;
Matches 63; Conservative 34; Mismatches 81; Indels 107; Gaps 10;

```
QY 54 YRQSLGQGPPEFLIYFQGTGAADDSGLPNDRFFAVRPEGSVSTLKIQTQEQDGAAYLRAG 113
Db 113 YTFQGYDGDDEFVSF-----DLKTESWTPVTEAVVTHKWDNDK-----G 152
QY 114 VAAGWSYNEQ-----YFGPGTGLTLVLEDIKNVFPPEVAVPEPSEAEISHTQKATLV 165
Db 153 LNAWGVNLTQNCPEWLKKYNYGR-----SSLMTVPVPSVSL-----LQMTSSSPVS 200
QY 166 CLATGFYPDHVELSWVNGKEVHSGVSTDPQPLKEQPALNDSRYCLSLRLRVSATFWQNP 225
Db 201 CYATGFYFNRAEMLWRKGDVTHDGVK-----EILPNDGTTFQMSVELTSLA----- 249
QY 226 RNHFRQVQFYGLSENDEWTDQRAKPVTOIVSAEANGRADCGFTSESYQQGVLSATILYE 285
Db 250 -----SEDMWKYDCVFOGLSGVDKDLV----- 270
QY 286 ILLGKA-----TLYAVLV---SALVLMAMVKRKDSR 313
Db 271 IPLDKANIKTNAGNSLALITLIVAVVLTISAVIVILVLRKKKAK 315

RESULT 12
Q9WTN4
ID Q9WTN4 PRELIMINARY; PRT; 509 AA.
AC Q9WTN4
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE BIT.
```


Search completed: October 11, 2000, 06:30:06
Job time: 1285 sec

Db 178 WKNYLEKEIEIWLQYVGYGR-----ETLBRKVPPTASVFQBEES-----SPEVYVCHAT 226
Qy 170 GFYDPHVELSWNGKVKHVSVDPLKEQPALNDSRYCLSRRLVRSATFWQNPNNHF 229
Db 227 GFFPKTYMITWQKDGEDVHEDE-----LRETLPNQDGTQKRSILTVSAEDLQ--KHTY 279
Qy 230 RCOVQFGLSENDEWTDRAKPTVQIVSAEAWGRADCGFTSESVOQGVLSATILYETILG 289
Db 280 TCVIQHSL-----KEMLPVSE-----RRILNPGGGGVVLIGIIVG 318
Qy 290 KATLYAVLVLSALVLMAMVKRKDS 312
Db 319 VVAALLVLVAVVAGIVVWKKKNS 341

RESULT 15

O46875
ID O46875 PRELIMINARY; PRT; 348 AA.
AC O46875;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE MHC CLASS IB ALPHA CHAIN PRECURSOR (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PVG.R19; TISSUE-SPLEEN;
RA Leong L.Y.W., Deverson E.V., Joly E., Butcher G.W.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y13890; CAA74192.1; .
DR HSSP; P01900; 1B11.
DR INTERPRO; IPR000495; .
DR INTERPRO; IPR001039; .
DR INTERPRO; IPR001064; .
DR INTERPRO; IPR003006; .
DR PFAM; PF00047; 1g; 1.
DR PFAM; PF00129; MHC_I; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Signal; MHC.
FT NON_TER 1 1
FT SIGNAL <1 3 POTENTIAL.
FT CHAIN 4 348 MATURE MHC CLASS IB ALPHA CHAIN.
SQ SEQUENCE 348 AA; 39108 MW; BD4C4D8880ED611E CRC64;

Query Match 8.5%; Score 142; DB 7; Length 348;
Best Local Similarity 25.9%; Pred. No. 2.5e-05;
Matches 75; Conservative 44; Mismatches 97; Indels 74; Gaps 15;

Qy 49 TALWYRQSLGQGPFLIYFGTGAADDGSL-----PNDRFFAVRPEGVSSTLKIQR 100
Db 83 TLLRYNQSEG-GSHTTQWMSGCDLGSGLLRGQESAYNGRDYIVLNE-----DLKT 135
Qy 101 TEQDQSAAYL-----RAGVAAGWSSYNEQYFGPGTRLTVL-----EDLNVPPE- 145
Db 136 WTAADTAARTIRNKWDRAERKAYLE-----GTCLESLLRYLELGETLLRSPPKA 190
Qy 146 -VAVFESEAEISHTQKATLVCLATGYPDHVELSWNGKVKHVSVDPLKEQPAL 204
Db 191 HVTLHPREPGDV-----TLRCWALGFYPAGISLTWOLNGED----LTQDMELVETRPA - 239
Qy 205 NDSRYCLSSRLVRSATFWQNPNNHFRCQVQFYGLSENDEWTDRAKPTVQIVSAEAWGRA 264
Db 240 GDGTFQKWSVVPPLGREQN---YTCLVEHEGLPE-----PLTQ-----RW 277
Qy 265 DCGFTSRYQGVLSATILYETILGKATLYAVLVLSALVLMAMVKRKDSRG 314
Db 278 EPSPSTDSN----METNVYIVLGAIVGAVIIAALVTIVR-KRRNTGG 322

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 11, 2000, 06:08:06 : Search time 15.62 Seconds
(without alignments)
687.378 Million cell updates/sec

Title: US-09-405-940-1

Perfect score: 1664

Sequence: 1 MGRLLCWALCLLGADHTG.....AVLSALVLMAMVKRDSRG 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36:*

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- 2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT:*
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- 21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1664	100.0	314	20 W99374	Human T-cell recep
2	1433	86.1	314	20 Y15229	Human receptor pro
3	1371	82.4	318	21 Y32208	Human receptor mol
4	1351	81.2	312	21 Y69988	Human receptor-ass
5	1273	76.5	345	21 Y69986	Human receptor-ass
6	1247.5	75.0	311	19 W47589	T-cell receptor be
7	1244	74.8	312	6 P50079	T-cell antigen rec
8	1244	74.8	312	7 P60471	Portion of a human
9	1230	73.9	312	15 R53145	T-cell antigen rec
10	1182	71.0	316	21 Y69999	Human receptor-ass
11	944	56.7	179	21 Y51069	Human TCRbeta prot
12	925.5	55.6	303	20 Y05403	Killer T-cell rece

13	907	54.5	177	21	Y51068
14	896	53.8	306	6	P50252
15	883	53.1	314	20	Y05728
16	880	52.9	287	21	Y56077
17	880	52.9	287	21	Y57853
18	880	52.9	306	6	P50344
19	874.5	52.6	307	21	Y56059
20	874.5	52.6	307	21	Y56083
21	874.5	52.6	307	21	Y57859
22	874.5	52.6	307	21	Y57868
23	873.5	52.5	287	21	Y56079
24	873.5	52.5	287	21	Y56081
25	873.5	52.5	287	21	Y57855
26	873.5	52.5	287	21	Y57857
27	870	52.3	287	21	Y56056
28	870	52.3	287	21	Y57865
29	870	52.3	305	21	Y56057
30	870	52.3	305	21	Y57866
31	870	52.3	306	21	Y56061
32	870	52.3	306	21	Y56085
33	870	52.3	306	21	Y57861
34	870	52.3	306	21	Y57870
35	869.5	52.3	307	21	Y56086
36	869.5	52.3	307	21	Y57862
37	868.5	52.2	293	7	P60238
38	868.5	52.2	293	10	P91815
39	868.5	52.2	293	18	W01532
40	868.5	52.2	293	21	Y50114
41	827	49.7	391	17	R97659
42	811	48.7	150	21	Y51072
43	736	44.2	173	21	Y51066
44	731	43.9	173	21	Y51067
45	621	37.3	146	21	Y51071

ALIGNMENTS

RESULT 1

W99374
ID W99374 standard; Protein; 314 AA.

XX
AC W99374;

XX
DT 21-MAY-1999 (first entry)

XX
DE Human T-cell receptor beta-like protein.

XX
KW T-cell receptor beta-like protein; antigen recognition; cancer;
autoimmune disorder; antagonist; diagnosis.

XX
OS Homo sapiens.

XX
PN W09903995-A1.

XX
PD 28-JAN-1999.

XX
PF 17-JUL-1998; 98WO-US14598.

XX
PR 18-JUL-1997; 97US-0897097.

XX
PA (INCY-) INCYTE PHARM INC.

XX
PI Corley NC, Hillman JL;

XX
DR WPI: 1999-132239/11.

XX
DR N-FSDB; X25736.

XX
PT New isolated T-cell receptor beta-like protein - used to develop
products for the diagnosis and treatment of cancer or autoimmune
disorders, e.g. AIDS, diabetes, infections or trauma

PS Claim 1; Fig 1A-D; 69pp; English.

Human TCRbeta prot
Sequence of T-cell
Mouse A1 T cell re
HLA-A2/flu restric
TCR beta chain and
Sequence encoded b
HTLV-1 Tax/HLA-A2
TCR beta chain and
TCR beta chain and
Mouse H2-Dd/flu nu
HLA-A2/HIV gag res
TCR beta chain and
TCR beta chain and
HLA-A2/flu restric
TCR beta chain and
HLA-A2/flu restric
HTLV-1 Tax/HLA-A2
TCR beta chain and
TCR beta chain and
HTLV tax/HLA-A2 re
TCR beta chain and
Sequence of the be
Mammalian T lympho
Cytotoxic T lympho
Murine cytotoxic T
Single chain T cel
Human TCRbeta prot
Murine TCRbeta pro
Murine TCRbeta pro
Murine TCRbeta pro

XX This sequence represents a new purified T-cell receptor (TCR) beta-like
 CC protein (TCRLP). The TCRLPs are essential to the formation of a
 CC functional TCR and play a role in antigen recognition by T cells.
 CC The TCRLP polypeptides and polynucleotides appear to play a role in
 CC cancer and autoimmune disorders. The TCRLP and agonists can be used for
 CC treating cancer. TCRLP antagonists can be used for treating autoimmune
 CC disorders, e.g. AIDS, Addison's disease, adult respiratory distress
 CC syndrome, allergies, anaemia, asthma, atherosclerosis, bronchitis,
 CC cholecystitis, Crohn's disease, ulcerative colitis, atopic dermatitis,
 CC dermatomyositis, diabetes mellitus, emphysema, erythema nodosum, atrophic
 CC gastritis, glomerulonephritis, gout, Graves' disease, hyperosinophilia,
 CC irritable bowel syndrome, lupus erythematosus, multiple sclerosis,
 CC myasthenia gravis, myocardial or pericardial inflammation, osteoporosis,
 CC osteoarthritis, pancreatitis, polymyositis, rheumatoid arthritis,
 CC scleroderma, Sjogren's syndrome, and autoimmune thyroiditis,
 CC complications of cancer, haemodialysis, and extracorporeal circulation.
 CC viral, bacterial, fungal, parasitic, protozoal, and helminthic infections
 CC and trauma. The products can also be used for detection, diagnosis and
 CC drug screening.
 XX
 SQ Sequence 314 AA;

Query Match 100.0%; Score 1564; DB 20; Length 314;
 Best Local Similarity 100.0%; Pred. No. 2.4e-144;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRLLCWAALCLLGGADHTGAGVSQTPSNKVKTEKGDVELRCDDPISGHTALYWRSLGQ 60
 DB 1 mgtrllcwaalcllggadhtgagvsqtpsnkvtekgdvelrcddpishgthalywyrslgq 60
 QY 61 GPFFLYFOGTGAADSGPLNDRFFAVRPEGSVSTIKIQRTQEGDSAAYLRAAGVAGWS 120
 DB 61 gpeflyfpgtgaadsgplndrfavrpelsgsvstikiqrtedgdsaaylragvagaWS 120
 QY 121 YNRYQYGPGRNLVLEDKNVFPEVAVPEPSAEISHTOKATVCLATGCFYDPDHVELSW 180
 DB 121 yneqyfgpgrnlvleldknvfpvavpsepsaeishtokatlvcLATGCFYDPDHVELSW 180
 QY 181 WVGKEVHSGVSTDPOPLKEQPALNDSRYCLSLRLVSATFWQNPFRHCQVQFYLSE 240
 DB 181 wvgkevhsqvstdpplkeqpallndsrYCLSLRLVSATFWQNPFRHCQVQFYLSE 240
 QY 241 NDEWTDQRAKPVTOIVSAEAWGADCGFSESQQOQVLSATILYELIGKATLYAVLVSA 300
 DB 241 ndewtdqrakpvtqvtsaeawgadcgftsyesyqqqvlsatillyelilgkatlyavlvsa 300
 QY 301 LVLMAWVKRRDSRG 314
 DB 301 lvlmawvkrkdsrg 314

RESULT 2

YI5229
 ID YI5229 standard; protein; 314 AA.
 AC YI5229;
 XX
 XX 26-OCT-1999 (first entry)
 DT Human receptor protein (HURP); 8 amino acid sequence.
 DE
 DE receptor; cancer; autoimmune disorder; inflammation;
 KW antagonist; cell surface protein; cell signalling;
 KW antibody; human receptor protein; HURP; reproductive disorder;
 KW developmental disorder; gastrointestinal disorder.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 205
 FT /note= "Potential N-glycosylation site"
 FT

FT Misc-difference 312 /note= "Potential cAMP-/cGMP-dependent protein-
 FT kinase phosphorylation site"
 FT Misc-difference 101 /note= "Potential casein kinase II-
 FT phosphorylation site"
 FT Misc-difference 133 /note= "Potential casein kinase II-
 FT phosphorylation site"
 FT Misc-difference 152 /note= "Potential casein kinase II-
 FT phosphorylation site"
 FT Misc-difference 239 /note= "Potential casein kinase II-
 FT phosphorylation site"
 FT Misc-difference 26 /note= "Potential protein kinase C-
 FT phosphorylation site"
 FT Misc-difference 81 /note= "Potential protein kinase C-
 FT phosphorylation site"
 FT Misc-difference 95 /note= "Potential protein kinase C-
 FT phosphorylation site"
 FT Misc-difference 159 /note= "Potential protein kinase C-
 FT phosphorylation site"
 FT Misc-difference 212 /note= "Potential protein kinase C-
 FT phosphorylation site"
 XX WO9941375-A2.
 XX 19-AUG-1999.
 XX 05-FEB-1999; 99WO-US02572.
 XX 12-FEB-1998; 96US-0022939.
 XX (INCY-) INCYTE PHARM INC.
 XX Au-Young J, Bandman O, Baughn M, Corley NC, Guegler KJ;
 XX Hillman JL, Lal P, Shah P, Tang YT, Yue H;
 XX WPT: 1999-494536/41.
 XX N-FSDB: 206373.
 PT New human receptor proteins, used e.g. to treat, prevent and
 PT diagnose gastrointestinal and developmental disorders - and related
 PT nucleic acids, vectors, transformed cells, antibodies, agonists and
 PT antagonists
 XX Claim 1; Page 85-86; 94pp; English.
 XX The Human receptor protein 8 (HURP-8) shares 87% identity with
 CC human T-cell receptor beta.
 CC HURP-8 is expressed in cancerous, inflamed, haematopoietic/immune
 CC and gastrointestinal tissue. HURP-4 therefore appears to have a role in
 CC some forms of cancer, inflamed, haematopoietic/immune and
 CC gastrointestinal disorders.
 CC This gives rise to the possibility of using an antagonist or an antibody
 CC of HURP to treat or prevent cancer or autoimmune/inflammatory disorders.
 XX
 SQ Sequence 314 AA;

Query Match 85.18; Score 1433; DB 20; Length 314;
 Best Local Similarity 85.6%; Pred. No. 3.1e-123;
 Matches 272; Conservative 12; Mismatches 30; Indels 0; Gaps 0;

QY 1 MGRLLCWAALCLLGGADHTGAGVSQTPSNKVKTEKGDVELRCDDPISGHTALYWRSLGQ 60
 DB 1 mgtrllcwaalcllggadhtgagvsqtpsnkvtekgdvelrcddpishgthalywyrslgq 60

QY	61	GPEFLYFGTGAADSGLPNDRFFAVFPEGSVSTLKIQTQEGDSNAYLRACVAGNWS	120
Db	61	gpeflyfneaqldksglpdrffaerpegsbstlklrtqgdsavylcass:spagv	120
QY	121	YNEQYFGPGTRITVLIEDLKNVFPPEVAVFEPSEAEISHTQATLVLCATGFPDHFVLSW	180
		:	
Db	121	vdqyfgpgtritvledlknvfppevavfepseaeishtqatlvclatgfpdhwls	180
QY	181	WVNGKEVHSGVSTDQPLKEQPALNDSYCLSSRLRVSATFWONPRNHRFCQVQFGLSE	240
Db	181	wvngkevhsgvstdbpqlkeqpalndsyrcylssrlrvsatfwnprnhrcqvqfvlse	240
QY	241	NDEWTODRAKPVTTQVSAEAWGRADCGFTSSYQOGLSATILYELLGKATLYAVLVSA	300
Db	241	ndewtdrkapvtqvsaawgradcgftssyqgglvatillyellgkatlyavlvsa	300
QY	301	LVLMMVYKRKDSRG 314	
Db	301	lvlmamvkrkdsrg 314	
RESULT	3		
Y32208			
ID	Y32208	standard; Protein; 318 AA.	
XX	AC	Y32208;	
XX	AC	XX	
XX	DT	15-FEB-2000 (first entry)	
XX	DE	Human receptor molecule (REC) encoded by Incyte clone 3428945.	
XX	KW	Receptor; REC; human; diagnosis; therapy; neoplastic disorder;	
XX	KW	immunological disorder; reproductive disorder; nervous disorder;	
XX	KW	gastrointestinal disorder; smooth muscle disorder;	
XX	KW	musculoskeletal disorder.	
XX	OS	Homo sapiens.	
XX	XX	WO95957270-A2.	
XX	PN	11-NOV-1999.	
XX	PD	28-APR-1999; 99WO-US09191.	
XX	PF	01-MAY-1996; 98US-0071822.	
XX	PR	(INCY-) INCYTE PHARM INC.	
XX	PA	Hillman JL, Bandman O, Tang YT, Yue H, Lal P, Corley NC;	
XX	PI	Guegler KJ, Patterson C;	
XX	PI	WPI; 2000-052971/04.	
XX	DR	N-PSDB; 234617.	
XX	DR		
XX	XX		
PT	PT	Novel human receptor molecules used in the diagnosis, treatment and	
PT	PT	prevention of neoplastic, immunological, reproductive gastrointestinal,	
PT	PT	nervous, smooth muscle and musculoskeletal disorders	
XX	XX		
PS	PS	Claim 1; Page 80-81; 94pp; English.	
XX	XX		
CC	CC	The present sequence represents a human receptor molecule (REC)	
CC	CC	encoded by Incyte cDNA clone 3428945. The invention provides human	
CC	CC	RECs and polynucleotides which identify and encode REC, as well as	
CC	CC	vectors, host cells, antibodies, agonists and antagonists. Human	
CC	CC	RECs appear to play a role in neoplastic, immunological,	
CC	CC	reproductive gastrointestinal, nervous, smooth muscle and	
CC	CC	musculoskeletal disorders. The protein, antagonists and agonists,	
CC	CC	and compositions can be used to treat: a reproductive disorder,	
CC	CC	including but not limited to, prolactin production disorders,	
CC	CC	infertility including tubal disease, ovulatory defects, endometriosis,	
CC	CC	disruptions of the estrous and menstrual cycles, polycystic ovary	
CC	CC	syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian	


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Db 178 lswvngkeivsgvstbqpikqepalndsrlyclssrlrvsatfwnprnfrqcvfyg 237
QY 238 LSEDEWTDQRAKPYTQIVSAEAWGRADCGFTSESYQGVLSATILYEILLGKATLYAVL 297
DB 238 lsewtdqdrakpvtqivsaeeawgracgftsvsyqgvlsatillyeillgkatlyavl 297
QY 298 VSALVLMAMVKRKD 311
DB 298 vsalvlmamvkrkd 311

RESULT 9
R53145
ID R53145 standard; Protein; 312 AA.
XX AC R53145;
XX DT 08-SEP-1994 (first entry)
XX DE T-cell antigen receptor.
XX KW T-cell antigen receptor; T-lymphocyte; probe; hybridization; MOLT-3.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 90 /note= "possible N-glycosylation site"
FT Misc-difference 205 /note= "possible N-glycosylation site"
XX EP593092-A..
XX PD 20-APR-1994.
XX PF 14-JAN-1985; 85EP-0118695.
XX PR 13-JAN-1984; 84US-0570694.
XX PR 06-FEB-1984; 84US-0577526.
XX PA (ONTA-) ONTARIO CANCER INST.
XX PI Mak TW;
XX WPI; 1994-127936/16.
XX DR N-PSDB; Q62128.
XX New nucleic acid encoding T-cell antigen receptor - is useful
PT e.g. as a probe to identify T-cells
XX Disclosure; Fig 3; 13pp; English.
XX mRNA complementary to the DNA sequence given in Q62128 is obtained by
CC isolating mRNA from MOLT-3 cells, preparing cDNA, inserting the cDNA
CC into the BglII site of vector pFP502BB5, transfecting the vector into
CC Escherichia coli HB101, and screening for 1.3 kb T-cell specific
CC mRNA in MOLT-3 and HSC-58 cells. The mRNA encodes a portion of the
CC T-cell antigen receptor (sequence R53145).
XX Sequence 312 AA;

Query Match 73.9%; Score 1230; DB 15; Length 312;
Best Local Similarity 76.8%; Pred. NO. 1.1e-104;
Matches 241; Conservative 21; Mismatches 46; Indels 6; Gaps 2;

QY 1 MGRRLICWALCLLGDHAGAGYSQTPSNKYTEKGDKDELRCDPISCHTALYWRQSLQ 60
DB 1 mdswtfcvscilvakhdagviqprhvevmgdevlrcckpishghnlsfsyrtqmmr 60
QY 61 GPEFLTYFOQTGAADSGLPNDRFFAVRPEGSYSTLKIQRTQEGDAAAYLRAGVAAGWSS 120
DB 61 glallyfnnnvpidsgmpedrfksakmpnasfstlikipseprdsavf---cassfst 117

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QY 121 YNEQY---FGPGRLTVLEDLKNVFPPEVAFPESEAEISHTOKATLVCLATGYPDHVE 177
DB 118 csanygytfgsgtrltvvedlnkvfppevafpseaeishtkatlvclatgfpdhve 177
QY 178 LSWWNGKEVHSGVSTDPOLKEQPALNDSRYCLSSRLRVSATFWQNPNRHFRQCVQFYG 237
DB 178 lswwngkevhsgvstbqpikqepalndsrlyclssrlrvsatfwnprnfrqcvfyg 237
QY 238 LSEDEWTDQRAKPYTQIVSAEAWGRADCGFTSESYQGVLSATILYEILLGKATLYAVL 297
DB 238 lsewtdqdrakpvtqivsaeeawgracgftsvsyqgvlsatillyeillgkatlyavl 297
QY 298 VSALVLMAMVKRKD 311
DB 298 vsalvlmamvkrkd 311

RESULT 10
Y69999
ID Y69999 standard; Protein; 316 AA.
XX AC Y69999;
XX DT 31-MAY-2000 (first entry)
XX DE Human receptor-associated protein from Incyte clone 2656082.
XX KW Human receptor-associated protein; HRAP; Incyte clone 2656082;
KW cytosolic; immunomodulatory; antiinflammatory; cardiac; antianemic;
KW antiasthenic; hepatotropic; antidiabetic; antirheumatic;
KW antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological;
KW neuroprotective; diagnosis; treatment; prevention; reproductive disorder;
KW cardiovascular; cell proliferative; autoimmune; inflammation; allergy;
KW gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;
KW arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis;
KW multiple sclerosis; irritable bowel syndrome.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1..22 /label= Signal_peptide
FT Protein 23..316 /label= Mature_HRAP
FT Domain 35..112 /label= Immunoglobulin-like_domain
FT Domain 161..235 /label= Immunoglobulin-like_domain
FT Domain /label= Immunoglobulin-like_domain
FT Domain 286..306 /label= Transmembrane_domain
FT Modified-site 26 /note= "Potential phosphorylation site"
FT Modified-site 35 /note= "Potential phosphorylation site"
FT Modified-site 39 /note= "Potential phosphorylation site"
FT Modified-site 57 /note= "Potential phosphorylation site"
FT Modified-site 69 /note= "Potential phosphorylation site"
FT Modified-site 135 /note= "Potential phosphorylation site"
FT Modified-site 154 /note= "Potential phosphorylation site"
FT Modified-site 161 /note= "Potential phosphorylation site"
FT Modified-site 214 /note= "Potential phosphorylation site"
FT Modified-site 241 /note= "Potential phosphorylation site"
FT Modified-site 314 /note= "Potential phosphorylation site"

```



```

DE  Killer T-cell receptor protein sequence.
XX
KW  Killer T-cell receptor; HIV; infection; HIV-1 IIIB; therapy.
OS  Mus musculus.
XX  WO9916885-A1.
PN  08-APR-1999.
PD
PF  28-SEP-1998; 98WO-JP04345.
PR  26-SEP-1997; 97JP-0262536.
XX  (KYOW ) KYOWA HAKKO KOGYO KK.
PA  (SAITO/) SAITO T.
XX  (TAKA/) TAKAHASHI H.
PI  Saito T, Takahashi H;
XX  WPI; 1999-255096/21.
DR  N-PSDB; X36391.
XX
XX  Killer T-cell receptor peptide specifically recognizing HIV-infected
PT  cells
XX
PS  Claim 7; Page 60-62; 75pp; Japanese.
XX
XX  This sequence is a killer T-cell receptor protein of the invention,
CC  which recognises and damages cells infected with human immunodeficiency
CC  virus (HIV), especially with HIV-1 IIIB. The receptor can be used as
CC  a constituent of compositions for the treatment of HIV infection.
XX
SQ  Sequence 303 AA;

Query Match      55.6%; Score 925.5; DB 20; Length 303;
Best Local Similarity 60.3%; Pred. No. 7.6e-77;
Matches 188; Conservative 34; Mismatches 81; Indels 9; Gaps 4;

QY  1 MTRILLWNAALCLLGADHFGAGVSTPNKNVTEKGDVLRCDPTSGHTALYWRQSLGQ 60
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  1 mgsrlf-fvllllcakhmeaavtgsrskvavtggkvltlshqtnndhmywyrqdtgh 59
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  61 GPEFLIFYFGTGAADSLPNDREFAVRPEGSVSTLKIQTQEQGDSAAVLRAGVAAGWSS 120
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  60 glrlrhysvvaadstekgdip-dgykasrpsqenfllelaslsqavf---cassegr 115
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  121 YNEQYFGPGTRLTVLEDLKNVPPPEVAVPEPSEAEISHTQKATLVCLATGFPDPDEVELSW 180
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  116 eaefgfgpqrtrltvledlrnvtppkvsifepskaeiankqkatlvclargffpdhvelsw 175
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  181 WYNGKEVHSGVSTDPQLKEQPALNDSRYCLSSRLRVSATFWQNPNNHFRQVQFYGLSE 240
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  176 wvngkevhsgvstdpqayke---snysylssrllrvsatfwnpnnhfrqvgfhgise 231
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  241 NDEWTQDRAKPTQTVSAPAWGRACGFTSESYQQGVLSATILYEILLGKATLYAVLVSA 300
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  232 edkwpgsgkptvtqnisaeaawgradcgttsasyhgvisatilyeillgkatlyavlvsg 291
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  301 LVLMAMVKRKDS 312
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  292 lvlmamvkkkns 303
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
Y51068
ID  Y51068 standard; protein; 177 AA.
XX
AC  Y51068;
XX
DT  22-MAR-2000 (first entry)
XX

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```

DE  Human TCRbeta protein fragment #1.
XX
KW  T cell receptor beta; TCRbeta; human; constant region;
XX  immunosuppressor.
OS  Homo sapiens.
XX  JP11302299-A.
PN  02-NOV-1999.
PD
PF  21-APR-1998; 98JP-01110607.
XX  21-APR-1998; 98JP-01110607.
PR  (KIRI ) KIRIN BREWERY KK.
PA
XX  WPI; 2000-075345/07.
DR
XX  T cell receptor beta chain constant region peptide - has
PT  immunosuppressing activity
XX
PS  Disclosure; Page 11; 15pp; Japanese.
XX
XX  This invention describes a novel polypeptide comprising substantially
CC  part or all of the constant region of T cell receptor beta chain
CC  (TCRbeta) and containing substantially no other regions of TCRbeta and
CC  having immunosuppressing activity. The TCRbeta requires no consideration
CC  of tissue-compatible antigen for the patient to be dosed nor of antigen
CC  specificity. This sequence represents a fragment of the human TCRbeta
CC  protein described in the method of the invention.
XX
SQ  Sequence 177 AA;

Query Match      54.5%; Score 907; DB 21; Length 177;
Best Local Similarity 97.7%; Pred. No. 1.8e-75;
Matches 172; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY  136 EDLKNVPPPEVAVPEPSEAEISHTQKATLVCLATGFPDPDHVELSWVNGKEVHSGVSTDP 195
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  1 edlnkvfppevavfepseaeishtqkatlvclatgffpdhvelswvngkevhsgvstdp 60
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  196 QPLKEQPALNDSRYCLSSRLRVSATFWQNPNNHFRQVQFYGLSENDEWTQDRAKPTQI 255
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  61 qlkeqpaldndryclssrlrvsatfwnpnnhfrqvgfyglisendewtqdrakptqi 120
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  256 VSAEAWGRACGFTSESYQQGVLSATILYEILLGKATLYAVLVSAALVLMAMVKRKD 311
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  121 vsaeawgradcgtftsyyqgvlsatilyeillgkatlyavlvsaalvlmamvkrkd 176
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 14
P50252
ID  P50252 standard; Protein; 306 AA.
XX
AC  P50252;
XX
DT  07-OCT-1991 (first entry)
XX
XX  Sequence of T-cell antigen receptor beta chain encoded by cDNA
DE  clone 86T1.
XX
XX  Diagnosis; site-directed therapy.
XX
OS  Homo sapiens.
XX
XX  Key      Location/Qualifiers
FH  Peptide 1..19
FT  /label= leader
FT  Region 20..117
FT  /label= variable
FT  Region 118..133

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FT Region /label=joining
 FT 134...306
 FT /label= constant
 FT Modified-site 36..38
 FT /note= Possible carbohydrate attachment site"
 FT Modified-site 75..77
 FT /note="as above"
 FT Modified-site 138..140
 FT /note="as above"
 FT Modified-site 200..202
 FT /note="as above"
 FT Modified-site 249..251
 FT /note="as above"
 XX
 PN W08503947-A.
 XX
 XX 12-SEP-1985.
 XX
 XX 28-FEB-1985; 85WO-US00367.
 XX
 XX 22-OCT-1984; 84US-0663809.
 PR 01-MAR-1984; 84US-0585333.
 PR 31-OCT-1984; 84US-0665988.
 XX
 PA (STRD) LELAND STANFORD UNI.
 XX
 XX Davis MM, Hedrick SM;
 PI
 XX WPI; 1985-249152/40.
 DR N-PSDB; N50280.
 XX
 XX New DNA sequences coding for T-cell antigen receptors or
 PT fragments - useful in diagnostic assays, affinity chromatography,
 PT site directed therapy and diagnosis
 XX
 PS Disclosure; Fig 2; 41pp; English.
 XX
 XX Mammalian T-cell receptors appear to be 80-90kdal heterodimers,
 CC which are disulphide linked, and composed of two distinct
 CC glycoproteins of about 40 to 50kd, referred to as the alpha- and
 CC beta- subunits (N50284, N50256; N50280, P50252 respectively). The
 CC chains may be divided up into regions associated with specific exons
 CC by analogy to immunoglobulins. Genes encoding helper T-cell antigen-
 CC specific receptor subunits alpha- and beta- (TH-Ag receptor, alpha-
 CC or beta-subunit) were isolated. For the beta-subunit three thymus-
 CC derived clones were obtd, designated 86T1, 86T3 and 86T5 (N50280-
 CC N50282). The inventors claim a DNA sequence of at least about 15nt
 CC present in the sequence of 86T1 (N50280) or T11 (N50284) joined to
 CC non-wild type DNA.
 XX
 XX Sequence 306 AA;
 SQ
 Query Match 53.8%; Score 896; DB 6; Length 306;
 Best Local Similarity 58.0%; Pred. No. 3.8e-74;
 Matches 181; Conservative 39; Mismatches 86; Indels 6; Gaps 3;
 QY 1 MGRLLCWAALCLLGDHDTGAGVSOTPSKNVTEKGDVELRCDPTSGHTALYWRSLGQ 60
 Db 1 mscrlllyslclvcltalmttkitspyllilgra-nksleceqhlghnamwykqsak 59
 QY 61 GPEFLYFGTGAADSGLPNDRTFVAVRPGSVSLTKIQTORTQGSAAAYLRAGVAAGWS 120
 Db 60 ppeImflyalkqlrlnetvps-rfipecpdskllilhisavdpedsavfycasshgqgvs 118
 QY 121 YNEQYFGGCTRLTVLEDLKNVFPBVAVRPESEAFISHTOKATLYCLATGVPDHLVSLW 180
 Db 119 gntlyfgegrlrvliivdlnvcpkvsifepskaelankqatlvclargfipdhvslw 178
 QY 181 WYNGKEVHSGVSTDPQPLKEQPALNDSRYCLSSRLRVSGATFWQPNRHFRCQVQYGLSE 240
 Db 179 wvngkevhsgvstdpqayke-----snyschlsrrvsatfwhnprnhrfrcvqvhgls 234

QY 241 NDEWTQDRAKPVTVQIVSAEAWGRADCGFTSEYQOGLSATILYEILGKATLYAVLVA 300
 Db 235 edkpegspkpvtnisaeawgradcgitsasyggvlsatilyllgkatlyavlvst 294
 QY 301 LVLMAWVRKDS 312
 Db 295 lvmamvkrkns 306
 RESULT 15
 Y05728
 ID Y05728 standard; Protein; 314 AA.
 XX
 AC Y05728;
 XX
 DT 19-JUL-1999 (first entry)
 XX
 DE Mouse Al T cell receptor beta chain.
 XX
 KW T cell receptor beta chain; mouse; transgenic animal;
 KW animal model; immunological tolerance; graft rejection;
 KW tissue grafting; neonatal intolerance; transplantation antigen;
 KW H-Y antigen.
 XX
 OS Mus musculus.
 XX
 PN W09916867-Al.
 XX
 PD 08-APR-1999.
 XX
 PF 30-SEP-1998; 98WO-GB02965.
 XX
 PR 01-OCT-1997; 97GB-0020888.
 XX
 PA (ISIS-) ISIS INNOVATION LTD.
 XX
 XX Cobbold SP, Waldmann H, Zelenika D;
 XX
 XX WPI; 1999-255090/21.
 DR N-PSDB; X25358.
 XX
 XX Transgenic non-human mammal having only CD4 positive T cells
 PT specific for at least one transplantation antigen, useful for
 PT studying immunological tolerance
 XX
 PS Disclosure; Page 35-36; 41pp; English.
 XX
 CC The present sequence represents the T cell receptor (TCR) beta
 CC chain from the Al CD4+ T cell clone isolated from CBA/Ca mice. The
 CC Al clone recognises the minor histocompatibility antigen H-Y
 CC present in male, but absent in female, mice. cDNA (see X25358)
 CC encoding the Al TCR alpha chain was obtained by RT-PCR (see
 CC also X25352-53), and was used in the construction of Al(M)
 CC transgenic mice. The invention relates to a transgenic animal
 CC model comprising TCR alpha and beta chains. It provides a
 CC genetically modified non-human mammal having a population of CD4
 CC positive T cells specific for one or a limited number of selected
 CC antigens, including at least transplantation antigen capable of
 CC rejecting a tissue transplant containing the transplantation
 CC antigen and, if applicable, the other selected antigens. The
 CC animal has TCR genes which encode a TCR specific for the
 CC transplantation antigen. The animal is useful for studying
 CC immunological tolerance, especially the mechanisms of tolerance to,
 CC and the rejection of, tissue grafts, and in pregnancy. The animals
 CC are also useful for testing agents for biological activity in
 CC promoting or reducing immunological tolerance.
 XX
 SQ Sequence 314 AA;
 Query Match 53.1%; Score 883; DB 20; Length 314;
 Best Local Similarity 58.7%; Pred. No. 6.1e-73;
 Matches 182; Conservative 33; Mismatches 87; Indels 8; Gaps 5;

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OM protein - protein search, using sw model

Run on: October 11, 2000, 06:08:11 ; Search time 12.56 Seconds
(without alignments)
419.030 Million cell updates/sec

Title: US-09-405-940-1
Perfect score: 1664
Sequence: 1 MGRLLCWAALCLLGADHTG.....AVLSALVLMVMVKRDSRG 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCUTS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1664	100.0	314	3	US-08-897-097-1
2	1394.5	83.8	311	3	US-08-897-097-3
3	1332	80.0	310	3	US-08-897-097-4
4	895	53.8	314	5	5434340-7
5	868.5	52.2	293	5	5189147-3
6	827	49.7	391	4	PCT-US95-15696-2
7	707	42.5	266	5	5175384-11
8	584.5	35.1	217	5	5189147-7
9	265	15.9	102	3	US-08-466-368-9
10	243.5	14.6	236	3	US-08-487-580-10
11	239	14.4	234	3	US-08-487-550-2
12	237	14.2	235	2	US-08-378-939-12
13	236.5	14.2	215	2	US-08-480-753-8
14	228.5	13.7	213	3	US-08-630-820-6
15	224	13.5	241	2	US-07-916-098A-56
16	222.5	13.4	232	1	US-08-704-744-80
17	222.5	13.4	239	3	US-08-487-550-6
18	220.5	13.3	214	1	US-08-458-516-12
19	220.5	13.3	274	1	US-08-256-964A-19
20	219	13.2	242	1	US-08-398-613A-56
21	219	13.2	242	1	US-08-398-612A-56
22	219	13.2	242	1	US-08-398-611A-56
23	219	13.2	242	2	US-08-491-334A-56
24	219	13.2	242	3	US-09-027-449-42
25	219	13.2	242	3	US-08-804-444A-42
26	216.5	13.0	218	2	US-08-887-352B-15
27	216.5	13.0	218	2	US-08-887-352B-17
28	216.5	13.0	218	2	US-08-887-352B-19

29 216.5 13.0 218 2 US-08-887-352B-24
30 213.5 12.8 237 1 US-08-398-612A-28
31 213.5 12.8 237 1 US-08-398-611A-28
32 213.5 12.8 237 2 US-08-491-334A-28
33 213.5 12.8 237 3 US-09-027-449-25
34 213.5 12.8 237 3 US-08-804-444A-25
35 213.5 12.8 238 1 US-08-398-613A-28
36 213 12.8 233 2 US-07-934-373C-25
37 213 12.8 233 3 US-08-437-642B-25
38 213 12.8 233 4 PCT-US93-07832-25
39 212.5 12.8 219 1 US-08-353-400-34
40 212.5 12.8 237 2 US-08-463-587A-25
41 212.5 12.8 237 2 US-08-463-667A-3
42 212.5 12.8 237 3 US-08-923-854-25
43 212.5 12.8 237 4 PCT-US91-09133-26
44 212.5 12.8 239 1 US-08-953-400-37
45 212 12.7 214 2 US-08-480-753-6

ALIGNMENTS

RESULT 1
US-08-897-097-1
; Sequence 1, Application US/08897097
; Patent No. 6054292
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: T-CELL RECEPTOR BETA-LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,097
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0346 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TONGTUT01
; CLONE: 983910
US-08-897-097-1

Query Match 100.0%; Score 1664; DB 3; Length 314;
Best Local Similarity 100.0%; Pred. No. 1e-169;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTRLLCWAALCLLGGADHTGAGYSQTPSNKVTETKGDVELRCDPISGHTALYWRQSLGQ 60
 DB 1 MSTRLLCWAALCLLGGADHTGAGYSQTPSNKVTETKGDVELRCDPISGHTALYWRQSLGQ 60
 QY 61 GPEFLIYFQGTGAADSGLPNDRFFFAVRPEGSVSTLKIQRTQEGDSAAYLKAGVRAAGWS 120
 DB 61 GPEFLIYFQGTGAADSGLPNDRFFFAVRPEGSVSTLKIQRTQEGDSAAYLKAGVRAAGWS 120
 QY 121 YNEQYFGPCTRLTVLEDLKNVFPPEVAVPEPSEAEISHTQKATLVCLATGFPDPHVELSW 180
 DB 121 YNEQYFGPCTRLTVLEDLKNVFPPEVAVPEPSEAEISHTQKATLVCLATGFPDPHVELSW 180
 QY 181 WNGKEVHSGVSTDPQPLKEQPALNDSRYCLSRRLVSATFWQNPNNHFRCCQVFGYGLSE 240
 DB 181 WNGKEVHSGVSTDPQPLKEQPALNDSRYCLSRRLVSATFWQNPNNHFRCCQVFGYGLSE 240
 QY 241 NDEWTDRAKPVTVQIVSAEAWGRADCGFTSESYQQGVLSATILYELLGKATLYAVLVSA 300
 DB 241 NDEWTDRAKPVTVQIVSAEAWGRADCGFTSESYQQGVLSATILYELLGKATLYAVLVSA 300
 QY 301 LVLAMVKKRDSRG 314
 DB 301 LVLAMVKKRDSRG 314

RESULT 2

US-08-897-097-3
 ; Sequence 3, Application US/08897097
 ; Patent No. 6054292
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: T-CELL RECEPTOR BETA-LIKE PROTEIN
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/897,097
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0346 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 311 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 1100182
 ; US-08-897-097-3

Query Match 83.8%; Score 1394.5; DB 3; Length 311;
 Best Local Similarity 85.4%; Pred. No. 6.3e-141;
 Matches 268; Conservative 14; Mismatches 29; Indels 3; Caps 2;
 QY 1 MSTRLLCWAALCLLGGADHTGAGYSQTPSNKVTETKGDVELRCDPISGHTALYWRQSLGQ 60
 DB 1 MSTRLLCWAALCLLGGADHTGAGYSQTPSNKVTETKGDVELRCDPISGHTALYWRQSLGQ 60
 QY 61 GPEFLIYFQGTGAADSGLPNDRFFFAVRPEGSVSTLKIQRTQEGDSAAYLKAGVRAAGWS 120
 DB 61 GPEFLIYFQGTGAADSGLPNDRFFFAVRPEGSVSTLKIQRTQEGDSAAYLKAGVRAAGWS 120
 QY 121 YNEQYFGPCTRLTVLEDLKNVFPPEVAVPEPSEAEISHTQKATLVCLATGFPDPHVELSW 180
 DB 121 YNEQYFGPCTRLTVLEDLKNVFPPEVAVPEPSEAEISHTQKATLVCLATGFPDPHVELSW 180
 QY 181 WNGKEVHSGVSTDPQPLKEQPALNDSRYCLSRRLVSATFWQNPNNHFRCCQVFGYGLSE 240
 DB 181 WNGKEVHSGVSTDPQPLKEQPALNDSRYCLSRRLVSATFWQNPNNHFRCCQVFGYGLSE 240
 QY 241 NDEWTDRAKPVTVQIVSAEAWGRADCGFTSESYQQGVLSATILYELLGKATLYAVLVSA 300
 DB 241 NDEWTDRAKPVTVQIVSAEAWGRADCGFTSESYQQGVLSATILYELLGKATLYAVLVSA 300
 QY 301 LVLAMVKKRDSRG 314
 DB 301 LVLAMVKKRDSRG 314

RESULT 3

US-08-897-097-4
 ; Sequence 4, Application US/08897097
 ; Patent No. 6054292
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: T-CELL RECEPTOR BETA-LIKE PROTEIN
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/897,097
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0346 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 310 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:

LIBRARY: GenBank
CLONE: 339012
US-08-897-097-4

Query Match 80.0%; Score 1332; DB 3; Length 310;
Best Local Similarity 81.7%; Pred. No. 3e-134;
Matches 254; Conservative 17; Mismatches 38; Indels 2; Gaps 1;

QY 1 MGRLLCWAALCLLGADHTGAGVSQTPSNKVKTEKGDVLRCDPISGHTALYRWYRSLGQ 60
DB 1 MGRLLCWAALCLLGADHTGAGVSQTPSNKVKTEKGDVLRCDPISGHTALYRWYRSLGQ 60
QY 61 GPEFLYFQGTGADDSGLNDRFFAVRPEGSVSTLKIQRTQEGDSSAAYLRAGVAAGWSS 120
DB 61 GPEFLYFQGTGADDSGLNDRFFAVRPEGSVSTLKIQRTQEGDSSAAYLRAGVAAGWSS 120
QY 121 YNEQYFGPGRTRLVLEDLKNVFPPEVAVPEPSEAEISHTOKATLVCLATGYDPDHVELSW 180
DB 120 YNEQYFGPGRTRLVLEDLKNVFPPEVAVPEPSEAEISHTOKATLVCLATGYDPDHVELSW 180
QY 181 WYNGKEVHSGVSTDPOPLKEDPALNDSRYCLSSRLRVSAFWQNPNNHFRFCQVGYGLSE 240
DB 181 WYNGKEVHSGVSTDPOPLKEDPALNDSRYCLSSRLRVSAFWQNPNNHFRFCQVGYGLSE 240
QY 241 NDEWTDQRAKPTQIVSAEAWGRADCGFTSESYQQGVLSATILYELLGKATLYAVILVSA 300
DB 241 NDEWTDQRAKPTQIVSAEAWGRADCGFTSESYQQGVLSATILYELLGKATLYAVILVSA 300
QY 301 LVLMAVKKRD 311
DB 301 LVLMAVKKRD 311

RESULT 4
5434340-7
; Patent No. 5434340
; APPLICANT: KRIMPENFORTH, PAULUS J.A.; BERNS, ANTONIUS J.M.
; TITLE OF INVENTION: TRANSGENIC MICE DEPLETED IN MATURE
; T-CELLS AND METHODS FOR MAKING TRANSGENIC MICE
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; FILING DATE: 27-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 280,218
; FILING DATE: 05-DEC-1988
; SEQ ID NO: 7
; LENGTH: 314
5434340-7

Query Match 53.8%; Score 895; DB 5; Length 314;
Best Local Similarity 58.7%; Pred. No. 1.5e-87;
Matches 182; Conservative 34; Mismatches 86; Indels 8; Gaps 3;

QY 3 TRLLCWAALCLLGADHTGAGVSQTPSNKVKTEKGDVLRCDPISGHTALYRWYRSLGQGP 62
DB 13 TRLLCWAALCLLGADHTGAGVSQTPSNKVKTEKGDVLRCDPISGHTALYRWYRSLGQGP 62
QY 63 EFLYFQGTGADDSGLNDRFFAVRPEGSVSTLKIQRTQEGDSSAAYLRAGVAAGWSSYN 122
DB 63 EFLYFQGTGADDSGLNDRFFAVRPEGSVSTLKIQRTQEGDSSAAYLRAGVAAGWSSYN 122
QY 123 EQYFGPGRTRLVLEDLKNVFPPEVAVPEPSEAEISHTOKATLVCLATGYDPDHVELSWV 182
DB 123 EQYFGPGRTRLVLEDLKNVFPPEVAVPEPSEAEISHTOKATLVCLATGYDPDHVELSWV 182
QY 183 NGKEVHSGVSTDPOPLKEDPALNDSRYCLSSRLRVSAFWQNPNNHFRFCQVGYGLSE 242
DB 183 NGKEVHSGVSTDPOPLKEDPALNDSRYCLSSRLRVSAFWQNPNNHFRFCQVGYGLSE 242
QY 243 EWTQDRAKPTQIVSAEAWGRADCGFTSESYQQGVLSATILYELLGKATLYAVILVSA 302
DB 243 EWTQDRAKPTQIVSAEAWGRADCGFTSESYQQGVLSATILYELLGKATLYAVILVSA 302

Db 245 KWPEGSPKPVTONISAEAWGRADCGITSASYHOGVLSATILYELLGKATLYAVILVSGLV 304
QY 303 LMAVKKRDS 312
DB 305 LMAVKKRNS 314

RESULT 5
5189147-3
; Patent No. 5189147
; APPLICANT: SAITO, HARUO; KRANZ, DAVID M.; ELSSEN, HERMAN N.;
; TONEGAWA, SUSUMU
; TITLE OF INVENTION: METEROIDIMERIC T LYMPHOCYTE RECEPTOR
; ANTIBODY
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/271,216
; FILING DATE: 14-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 666,988
; FILING DATE: 31-OCT-1984
; APPLICATION NUMBER: 620,122
; FILING DATE: 13-JUN-1984
; SEQ ID NO: 3
; LENGTH: 293
5189147-3

Query Match 52.2%; Score 868.5; DB 5; Length 293;
Best Local Similarity 57.9%; Pred. No. 9.4e-85;
Matches 175; Conservative 34; Mismatches 82; Indels 11; Gaps 3;

QY 11 LCLLGADHTGAGVSQTPSNKVKTEKGDVLRCDPISGHTALYRWYRSLGQGPFLIYFQG 70
DB 3 LCLLGADHTGAGVSQTPSNKVKTEKGDVLRCDPISGHTALYRWYRSLGQGPFLIYFQG 70
QY 71 TGAADDSGLNDRFFAVRPEGSVSTLKIQRTQEGDSSAAYLRAGVAAGWSSYNEQYFQGT 130
DB 71 TGAADDSGLNDRFFAVRPEGSVSTLKIQRTQEGDSSAAYLRAGVAAGWSSYNEQYFQGT 130
QY 131 RTVLVLEDLKNVFPPEVAVPEPSEAEISHTOKATLVCLATGYDPDHVELSWVNGKEVHSG 190
DB 131 RTVLVLEDLKNVFPPEVAVPEPSEAEISHTOKATLVCLATGYDPDHVELSWVNGKEVHSG 190
QY 191 VSTDPOPLKEDPALNDSRYCLSSRLRVSAFWQNPNNHFRFCQVGYGLSENDEWTDQRAK 250
DB 191 VSTDPOPLKEDPALNDSRYCLSSRLRVSAFWQNPNNHFRFCQVGYGLSENDEWTDQRAK 250
QY 251 PVTQIVSAEAWGRADCGFTSESYQQGVLSATILYELLGKATLYAVILVSAVILVMAVKKR 310
DB 251 PVTQIVSAEAWGRADCGFTSESYQQGVLSATILYELLGKATLYAVILVSAVILVMAVKKR 310
QY 311 DS 312
DB 292 NS 293

RESULT 6
PCR-US95-15696-2
; Sequence 2, Application PC/TUS9515696
; GENERAL INFORMATION:
; APPLICANT: President and Fellows of Harvard College
; TITLE OF INVENTION: SINGLE CHAIN T-CELL RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:


```

: TITLE OF INVENTION: DNA ENCODING THE T CELL SURFACE PROTEIN
:
: TITLE OF INVENTION: T4 AND USE OF FRAGMENTS OF T4 IN THE TREATMENT OF AIDS
:
: NUMBER OF SEQUENCES: 21
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: Cooper & Dunham LLP
:
: STREET: 1185 Avenue of Americas
:
: CITY: New York
:
: STATE: New York
:
: COUNTRY: USA
:
: ZIP: 10036

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,368
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCES/DOCKET NUMBER: 24577-El-B/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400

RELREF: 212391-0329
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FEATURE:

US-08-466-368-9

Query Match 15.9%; Score 265; DB 3; Length 102;
Best Local Similarity 56.5%; Pred. No. 5.5e-21;
Matches 52; Conservative 12; Mismatches 28; Indels

QY	21	AGVSTPSNKVTEKGDVELRCOPISGHTALYWYRQSLGQPEFLIIFQGTGAADSGLP	80
		: : : : :	
Db	2	AGVIQSPRHVEVTMGQEVTLCKPISGHNSLFWYRQTMMRGLELLYFNNNVPIDDSGMP	61

Qy 81 NDRFFAVRPEGSVTLKIQRTTEGQDSAAYLRA 112
 ||| | | | ||||| : ||| | |
 Db 62 EDRESAKMPNASFSLKIQPSEPRDSAVYFCA 93

RESULT 10
US-08-487-550-10
; Sequence 10, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:

APPLICANT: ARSON, DARRELL R.
 TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
 TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
 TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
 TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 STREET: 699 Prince Street
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22314

COMPUTER READABLE FORM:

```

: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,550
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
:

```

```

NAME: IESKIN, ROOHI L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-10

```

Query Match 14.6%; Score 243.5; DB 3; Length 236;
Best Local Similarity 34.4%; Pred. No. 4.1e-18;
Matches 77; Conservative 31; Mismatches 77; Indels 39; Gaps 12;

Qy 23 VSOTPSNKVTEKGDVELRCDPISGHTA-----LYWYRSLGQGFEFLIYFQGTGAADD 76
||| ||| : | : | : ||| : ||| : ||| :
Db 30 VSCAPGQKV-----ISC---TGSTSNIGGYDLHWYQQLPGTAPKLLIY-----DI 72

Qy 77 SGLP---NDRFFAVRPEGSYSTLKIQTEQGDAAAYLRAGVAAGWSSYNEQYFGCGTRLT 133

Db 73 NRPSGISDRFSGSK-SGTAASLATGLQTEADYTCQSYD---SSLNAQVFGGGTRLT 128

QY 134 VLEDLKNVFPPEVAVFEPSEAEISHIQKATLYCLATGYPDPHVLSWVNGKEVHSGVST 193
|| | | | | : ||||| : ||| : |||
Dd 129 VLGPAA--PSVTFLPPSSEL-QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185

QY 194 DPQLKEQPALNDSRYCLSSRLRVSATFWQPNRNHRCQVQFYG 237
| | : : : | | | : : | : : | |
Db 186 -TPSKO---SNKYAASSYLSTPEOWKSHRS-YSCOVTHGE 223

RESULT 11
US-08-487-550-2
; Sequence 2, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

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: ZIP: 22314
:
: COMPUTER READABLE FORM:
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: MEDIUM TYPE: Floppy disk
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: COMPUTER: IBM PC compatible
:
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/08/487,550
:
: FILING DATE: 07-JUN-1995
:
: CLASSIFICATION: 435
:
: ATTORNEY/AGENT INFORMATION:
:

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Matches	73:	Conservative	42:	Mismatches	94:	Indels	35:	Gaps	12:
Qy	23	VSOTPSNKNVTEKGDVBLRCDPI	SGHTALWYRQSLGQGP	FLIYFQGTGAADSG	LPLND	82			
		:	:	:	:	:	:		
Db	5	MTQSPSSLASVSGDRVIT	ITCSTSSSVYMHWYQK	PKGAPKLLIYST	SNLA--	SGVPSR	61		
		:	:	:	:	:	:		
Qy	83	RFTAVRPGSVSLIKIORT	EGDSAAALRAGVAGNS	SYNEQYFGPGTRIT	LVLEDLKNVF	142			
		:	:	:	:	:	:		
Db	62	--FSGSGGGDFTTIS	SLQPEDIATV----	YCHWGSY--	PTEGQGTK--	VGIKRTVA	110		
		:	:	:	:	:	:		
Qy	143	PPEVAVPEPGEAEISH	QKATLVCLATGYF	PDHVELSWVNGKEV	HGVSVDTPQLR	EQP	202		
		:	:	:	:	:	:		
Db	111	APSVFIPEPPDEQIK	-SGTASVCLLN	NNFYPREAKVQ	WKVD-NALQSGNS-	-QESVTEQD	166		
		:	:	:	:	:	:		
Qy	203	ALNDSRYCLSLRSLRV	SATFQWQNP	RHPRFCOVQFVGL	SENDEWTDRAK	PVQIYSAEWG	262		
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Db	167	S-KDSTVSLSTLTSL	KADIYK-HKVACEV	THUGLS-----	SPVI-----	KSFN	209		
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Qy	263	RADC	266						
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Db	210	RGEC	213						

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RESULT 15
US-07-916-098A-56
; Sequence 56, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, JOSEPH D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916, 098A
; FILING DATE: July 24, 1992

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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: NO. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION NUMBER: 424 07/618,542
FILING DATE: NO. 5871732ember 27, 1990
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,310-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

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